Wed Nov 30 10:27:02 2005

Whiteman, B.	10/696900 Page 1	

 112.2 78.5 4722 13 AF028705 111.6 78.0 4721 6 CQ972062 111.6 78.0 4721 6 CS073592 111.6 78.0 4721 6 AX753246 A	23 111.6 78.0 4721 13 AF513851 24 107.4 75.1 145 6 A66401	n m	107.4 75.1 165 6 AR223306 107.4 75.1 165 6 AR58389 107.4 75.1 165 6 AR658389 107.4 75.1 165 6 AX106702	107.4 75.1 207 6 AA7/03496 107.4 75.1 272 6 AB221818 107.4 75.1 272 6 AB223305	107.4 75.1 27.2 AX105701 107.4 75.1 216 13 AA2LEFT	107.4 75.1 4675 6 BD094552 107.4 75.1 4675 6 AX135805	107.4 75.1 4675 6 AX286292 107.4 75.1 4675 6 AX783252 107.4 75.1 4675 6 AX783252	107.4 75.1 4679 13 AP043303	ALIGNMENTS	RESULT 1 BD242766 LOCUS BD242766 LOCUS BD242766 AT18 bp DEFINITION Adeno-associated virus serum type 1 nucleic acid sequence, vector	;	S	unclassified. REFERENCE 1 (bases 1 to 4718) AUTHORS Wilson,J.M. and Xiao,W. TITE: Adan-associated virus serum type 1 mucleic acid seguence. Vector	and host cell containing the same Patent: JP 2002529098-A 1 10-SEP-2002; THE TRUGITES OF THE UNIVERSITY OF PENNSYLVANIA	8 Z G	PR 05-NOV-1999 JP 2000581227 PR 05-NOV-1998 US 60/107114 PI JAMES M WILSON WEIDONG XIAO	C12N1/21, C12N5/10,C12P21/02//A61K35/76,C12N15/00,C12N5/00 CC eno-associated virus serum type 1 nucleic acid sequence, CC	vector and host CC cell containing the same	FH Key Location/Qualifiers FT CDS (335). (2206) FT CDS (2223). (4430).	FEATURES Location/Qualifiers 14718 Source /		. 40 00 0	Query Match 100.0%; Score 14.5; UB 5; Length 4/10; Best Local Similarity 100.0%; Pred. No. 2.5e-21;
GenCore version 5.1.6 Copyright (c) 1993 - 2005 Compugen Ltd.	OM nucleic - nucleic search, using sw model	Run on: November 28, 2005, 12:51:27 ; Search time 522.566 Seconds (without alignments) 15555.198 Million cell updates/sec	Title: US-10-696-900-1_COPY_1_143 Perfect score: 143 Sequence: 1 ttgcccactccctctgcgaactccattaggggtaa 143	Scoring table: IDENTITY NUC Gapop 10.0 , Gapext 1.0	Searched: 5883141 segs, 28421725653 residues	Total number of hits satisfying chosen parameters: 11766282	Minimum DB seq length: 0 Maximum DB seq length: 2000000000	Post-processing: Minimum Match 00% Maximum Match 100% Listing first 45 summaries		7: gb in: 3: gb_env: 4: gb_om: 5: gb_ov: 6: gb_ov: 7: gb	 	0 4 2	E 4. R	Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.	SUMMARIES	Query Score Match Length DB ID	1 143 100:0 4718 6 AES2498 AES52498 Sequence 3 143 100:0 4718 6 AES52498 AES52498 Sequence 4 143 100:0 4718 6 AES52498 AES52498 Sequence 5 143 100:0 4718 13 AF063497 AF063497 AE063497 AGENCASE	138.8 97.1 4683 13 AF028704 AF028704 137.2 95.9 4683 6 BD242775 A	7 137.2 95.9 4683 6 AR562507 8 135.6 94.8 4721 6 C0972062 9 135.6 94.8 4721 6 CS073492	10 135.6 94.8 4721 6 AX753246 AX753246 11 135.6 94.8 4721 13 AF513851 AF51385	119 83.2 4718 6 BD242766 BD242766 1 119 83.2 4718 6 AR562498 AR562498 4 119 83.2 4718 6 AX753251 AX753251 AX753251	15 119 83.2 4718 13 AF063497 AF06349 16 113.2 79.2 4722 13 AF028705 AF02870	7 113.2 79.2 4726 6 8 113.2 79.2 4726 13

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Mison, J.M. and Xiso, W.
Adeno-associated virus serotype 1 nucleic acid sequences, vectors
and host cells containing same
patent: 10 & 675927-A 1 06-JUL-2004;
The Trustees of the University of Pennsylvania; Philadelphia, PA
Location/Qualifiers
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Adeno-associated virus 1
Viruses; ssDNA viruses; Parvoviridae; Parvovirinae; Dependovirus.
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24 capteance 1 from patent US 6759237.

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aguence 6 from Patent BP1310571.
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Adeno-associated virus 1
Adeno-associated virus 1
Viruses; saDNA viruses; Parvoviridae; Parvovirinae; Dependovirus. 1 (1 (2008) 1 to 4718)
Xiao, W., Chirmule, N., Berta, S.C., McCullough, B., Gao, G. and Wilson, J.M.
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Xiao, W. and Wilson, J.M.
Direct Submission
Submitted (05-MAY-1998) IHGT, University of Pennsylvania, 3601
Spruce Street, Philadelphia, PA 19104, USA
Location/Qualifiers
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J. Virol. 73 (5), 3994-4003 (1999)
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Length 4718;
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100.0%; Score 143; DB 6; 100.0%; Pred. No. 2.5e-21;
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Rutledge E.A. and Russell, D.W.
Direct Submitssion
Submitted (24-SEP-1997) Hematology, Univ. of Washington, Box 357720, Seattle, WA 98195, USA
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100.0%; Pred. No. 2.5e-21;
tive 0; Mismatches 0;
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JAMES M WILSON, WEIDONG XIAO
CI2N15/09, A61K31/711, A61K48/00, A61P43/00, C12N1/15, C12N1/19, PC
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Wilson,J.M. and Xiao,W.
Wilson,J.M. and Xiao,W.
Adeno-associated virus serum type 1 nucleic acid sequence, vector and host cell containing the same
Patent: JP 2002529098+A 10 10-SEP-2002;
THE TRUSTEES OF THE UNIVERSITY OF PENNSYLVANIA
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/organism='aav-6'.
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/organism="unidentified"
/mol_type="genomic DNA"
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Wilson, J.M., Gao, G., Alvira, M.R. and Vandenberghe, L.H.
Adeno-associated virus (aav) clades, sequences, vectors containing
same, and uses therefor
Patent: Wo 2005033121-A 180 14-APR-2005;
The Trustees of the University of Pennsylvania (US)
Location/Qualifiers
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                                                                                                                                        Score 135.6; DB 6; Length 4721;
Pred. No. 9.8e-20;
0; Mismatches 4; Indels 0;
Patent: WO 2004108922-A 7 16-DEC-2004;
The Trustees of The University of Pennsylvania (US)
Location/Qualifiers
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                                               1. .4721
Organism="Adeno-associated virus"
/mol_type="unassigned DNA"
/db_xref="taxon:272636"
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CS073592

    .4721
    /organism="unidentified"
    /mol_type="unassigned DNA"
    /db_xref="taxon:32644"

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Sequence 1 from Patent EP1310571.
AX752246 GI:32166105
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Best Local Similarity 97.2%;
Matches 138; Conservative C
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Methods and compositions for lowering total cholesterol levels and
treatment of heart disease
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Mison,J.M. and Xiao,W.
Adeno-associated virus serotype 1 nucleic acid sequences, vectors and host cells containing same
and host cells containing same
Patent: US 6759327-A 19 06-JUL-2004;
The Trustees of the University of Pennsylvania; Philadelphia, PA
Location/Qualifiers
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                                               Score 137.2; DB 6;
Pred. No. 4.4e-20;
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Sequence 7 from Patent W02004108922.
CQ972062.
CQ972062.1 GI:57163375
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                                                                              0; Mismatches
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Sequence 19 from patent US 6759237.
AR562507
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/organism="unknown"
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   /db_xref="taxon:32644"
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Adeno-associated virus
                                             Query Match
Best Local Similarity 97.9%;
Matches 139; Conservative
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MVLGRFLSQIREKLVQTIYRGVEPTLPNWFAVTKTRNGAGGGNKVVDECYIPNYLLPK
TQPELQWANTNMEEYISACLALAERKRLVAQHLTHVSGTQEGNKENLAPNSDAPVIRS
TKSARYMELVGWLVDRGITSEKQMIQBODASYISFNAASNSRSQIKAALDNAGKIMALI
TKSARPDYLVGPSLPADIKTNRIYRILELNGYDPAYAGSYFLGWAQKKFGKRNTHWLFG
PATTGKTNIAEAIAHAVPFYGCVNWTNENFPFNDCVDKWVIWWEEGKMTAKVVESAKA
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/db_xref="G1:22652861"
/trānalation="MAADGYLPDWLEDNLSEGIREWWDLKPGAPKPKANQQKQDNGRG
/trānalation="MAADGYLPDWLEDNLSEGIREWWDLKPGAPKPKANQQKQDNGRG
RUPGYKYKIGPPNGLDKGEPVNAADAAALEHDKAYDQQLKAGDNPYLRYNHADBEFQE
RLQEDTSFGGNLGRAYFQAKKKYLEPLGLVEEGAKTARAKKRPVEPSPQRSPDSTGI
GKKGQQPARKKRLNFGQTGDSESVPDPQPLGEPPAAPSSVGSGTVAAGGGAPMADNNEG
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                                                                                                                                            ILGGSKVRVDQKCKSSAQIDPTPVIVTSNTNMCAVIDGNSTTFEHQOPLQDRMFKFEL
TIRGENDFKTVTKQEVKEFFRRASDIVTVEVAHEFFYVRKGASKRRAPDDDLDISEBRRA
CPSVADDSTSDAEGAPUDFADRYQNKCSRHAGNIQMLPPCKTCERANQNPNICFTHGV
RDCLECFPGVSESQPVVRKKTYRKLCAIHHLLGRAPEIACSACDLVNVDLDDCVSEQ"
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Wilson,J.M. and Xiao,W.
Adeno-associated virus serum type 1 nucleic acid sequence, vector and host cell containg the same Patent: JP 200529998-A 1 10-SEP-2002;
THE TRUSTEES OF THE UNIVERSITY OF PENNSYLWANIA
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C12N5/10,C12P21/02//A61K35/76,C12N15/00,C12N5/00
                                                                                                                                                                                                                                                                    2222. .4435
/note="similar to AAV2 VP1 protein"
                                                                                                                                                                                                                                                                                                                                                        'product="capsid protein"
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JAMES M WILSON, WEIDONG XIAO
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10-SEP-2002
02-NOV-1999 JP 2000581227
05-NOV-1998 US 60/1071:
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JP 2002529098-A/1.
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BD242766/c
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LNLIEQAPLTVAEKLQRDFLVQWRRVSKAPEALFFVQFEKGESYFHLHVLVETTGVKS
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Submitted (20-MAY-2002) Institute for Human Gene Therapy,
University of Pennsylvania, M6.40 Maloney Bldg, 36th & Spruce Sts,
Philadelphia, PA 19104, USA
Location/Qualifiers
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Adeno-associated virus 7
Viruses; ssDNA viruses; Parvoviridae; Parvovirinae; Dependovirus.
1 (bases 1 to 4721)
Gao, G.P., Alvira, M.R., Wang, L., Calcedo, R., Johnston, J. and
                                      Adeno-associated virus 7
Adeno-associated virus 7
Viruses; ssDNA viruses; Parvoviridae; Parvovirinae; Dependovirus.
                                                                                                                                                  Gao,G., Wilson,J.M. and Alvira,M.
A method of detecting and/or identifying adeno-associated virus
(AVV) sequences and isolating novel sequences identified thereby
Patent: EP 1310571-A 1 14-MAY-2003,
The Trustees of The University of Pennsylvania (US)
Location/Qualifiers
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/note="similar to AAV2 Rep 78 protein"
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/organism="Adeno-associated virus 7"
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|organism="Adeno-associated virus 7"
|mol_type="unassigned DNA"
|db_xref="taxon:202812"
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/product==nonstructural protein"
/protein_id="AAN03854.1"
/db_xref="GI:22652860"
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Pred. No. 9.8e-20;
0; Mismatches 4
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/specific_host="rhesus monkey"
/db_xref="taxon:202812"
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Best Local Similarity 97.2%;
Matches 138; Conservative 0
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Alvira,M.R.
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/codon_start=1
/product="nonstructural protein"
/protein_id="AAD27758.1"
/dp.rtef="GI:468908"
/translation="MPGFYEIVIKVPSDLDEHLPGISDSFVSWVAEXEWELPPDSDMD
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YVGRFLSGY IBDKLVQTI YRGIEPTLENWFAVTRRNGAGGARKVVDECY IBVKTLPK
TOPELOWAMTNMESY IS ACLIALAERKRLVACHLTHVSQTGEONKENLAPNSDEPVIRS
KTSARYMELVGWLVORGITSEKQMIQEDQASY ISFNAASNSRSQIKAALDNAGKIMAL
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Adeno-associated virus 1
Viruses; seDNA viruses; Parvoviridae; Parvovirinae; Dependovirus.
1 (bases 1 to 4718)
Xiao,W., Chirmule,N., Berta,S.C., McCullough,B., Gao,G. and Wilson,J.M.
                                                                                                                                                                        Gao,G., Wilson,J.M. and Alvira,M. A method of detecting and/or identifying adeno-associated virus A method of detecting and/or identifying adeno-associated virus (AVV) sequences and isolating novel sequences identified thereby Patent: EP 1310571-A 6 14-MAY-2003; The Trustees of The University of Pennsylvania (US) Location/Qualifiers
                                                                                                  Adeno-associated virus 1
Viruses; ssDNA viruses; Parvoviridae; Parvovirinae; Dependovirus
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Xiao, W. and Wilson, J.M.
Direct Submission
Submitted (ission
Sylver Street, Philadelphia, PA 19104, USA
Location/Qualifiers
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/mol_type="genomic DNA"
/db_xref="taxon:85106"
                                                                                                                                                                                                                                                                                                                               Adeno-associated virus 1, complete genome. AF063497
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89.5%; Pred. No. 3.7e-16;
tive 0; Mismatches 15;
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  AX753251
AX753251.1 GI:32166108
                                                                           Adeno-associated virus
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AF063497/c
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Wilson, J.M. and Xiao, M.
Malson, J.M. and Xiao, M.
Adeno-associated virus serotype 1 nucleic acid sequences, vectors
and host cells containing same
Patent: US 6759237-A 1 06-JUL-2004;
The Trustees of the University of Pennsylvania; Philadelphia, PA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  4718 TIGCCCACTCCCTCTCTGCGCGCTCGCTCGGTGGGGCCCGGCAGAGCAAGCTCTGC
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  Adeno-associated virus serum type 1 nucleic acid sequence,
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                                                                                                                                                                                                                                                                                                                               DB 6; Length 4718;
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Best Local Similarity 89.5%; Pred. No. 3.7e-16;
Matches 128; Conservative 0; Mismatches 15.
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                                                                                             (335). (2206)
(2223). (4430).
Location/Qualifiers
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6759237.
                                                                                                                                                                                                  /organism="unidentified"
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                                                                                                                                                                                                                            /mol_type="genomic DNA"
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                         vector and host
cell containing the same
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Sequence 1 from patent US 675
AR562498
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Unclassified.
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AR562498/c
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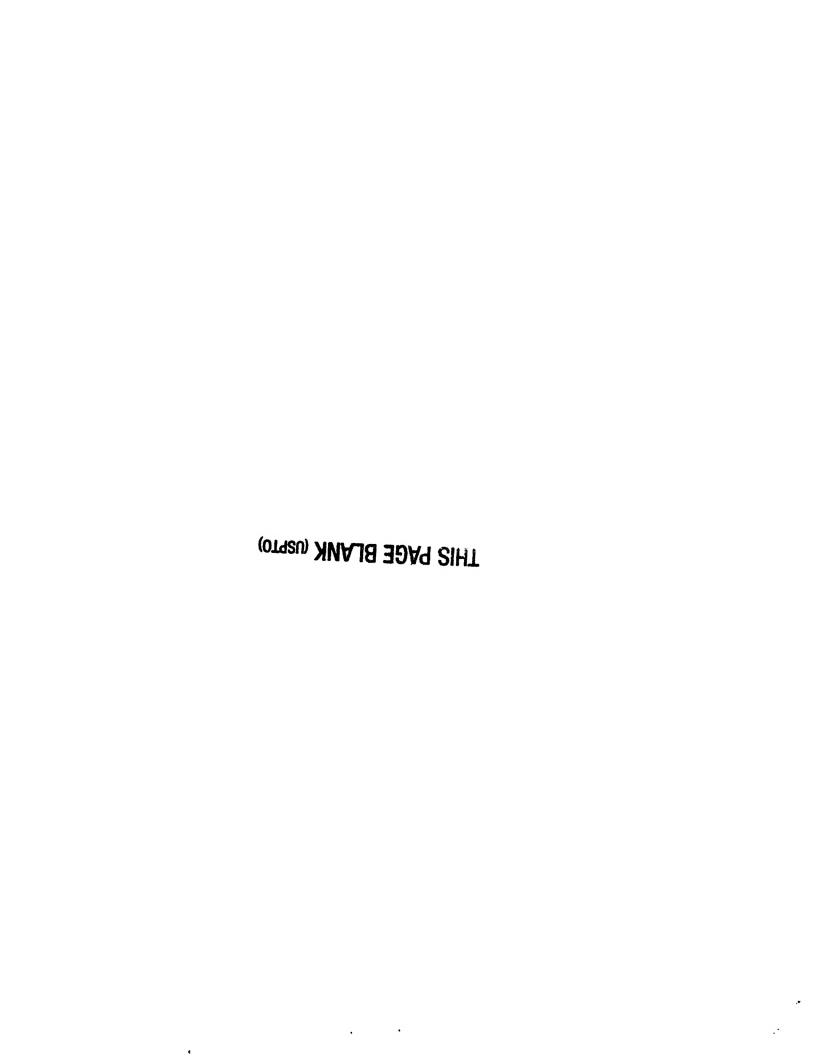
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ORIGIN

Search completed: November 29, 2005, 00:05:25 Job time : 524.566 secs

4598 GGCAACTCCATCACTAGGGGTAA 4576

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Ad113985 Adeno-ass
Adg3759 AAV-3A ge
Adg3748 AAV-3B DNA
Adg39760 AAV-3B Ge
Ade75502 Adeno-ass
Adv67509 Nucleotid
Adz27030 Adeno-ass
Aa41448 AAV2 inve
Aat03385 Strict in
Aax34295 Adeno-ass
Abs69884 Human ade
Ac58491 Adeno-ass
Ac58476 AAV-2 lef
Adv93250 Inverted
Aav33250 Inverted
Aav34568 Adeno-ass
Aa66769 Double-D
Aat49462 Adeno ass
Aa603535 Inverted
Abs69866 Human ade
Abs7176 Haad-to-t
Ad191189 Adeno-ass
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/*tag= c
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AAT49462
AAD03535
ABS69886
ABV77279
ADL91189
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AAD03534
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Aad60572 Adeno-ass
Ad13984 Adeno-ass
Ad13984 Adeno-ass
Ad39758 AAV-1 gen
Ad139976 AAV-6 gen
Ad39763 AAV-6 gen
Ad39764 AAV-7 gen
Ad40772 Adeno-ass
Ad60772 Adeno-ass
Ad60772 Adeno-ass
Ad13984 Adeno-ass
Ad339768 AAV-1 gen
Ad27507 Adeno-ass
Ad33976 AAV-3 Ben
                                                                                                                               November 28, 2005, 08:46:14; Search time 66.9124 Seconds (without alignments) 14243.261 Million cell updates/sec
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                           GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.
                                                                                                                                                                                                                                                                                                                                                               Total number of hits satisfying chosen parameters:
                                                                                                                                                                                                                                                                                                                            4996997 seqs, 3332346308 residues
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Maximum Match 100%
Listing first 45 summaries
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AAF23749
ADG13983
ADG139763
ADG39764
ADG39764
ADG27030
ADD0772
ADD73984
ADG39758
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                                                                                               - nucleic search, using sw model
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Gapop 10.0 , Gapext 1.0
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4718 4683 4683 4683 4721 4721

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143 138.8 138.8 135.6 135.6 135.6

119 119 113.2 113.2

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Length

Query

Score

Result Š.

122::::

Post-processing:

Database

Scoring table: Perfect score:

Searched:

Sequence:

Title:

OM nucleic

Wilson JM, Xiao W; WPI; 2000-376571/32

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1875. .1876
/tags q /note= "P40_RNA"
//tags 1974. .2220
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                notes "This region interrupts the coding sequence of Rep 8 and Rep 40"
223. .4433
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4576. .4718
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forming T-shaped hairpin structure"
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4447 ..4452
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634. 4433
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label= P5_TATA-Box
 label= P5_promoter
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/note= "P19 RNA"
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            237. .245
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           protein_bind
                                                                                     misc_feature
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The patent discloses an adeno-associated virus serotype 1 (AAV-1) DNA which is characterised by two inverted terminal repeats (ITR) and open reading frames for rep and capsid (cap) proteins. The rep reading frame encodes four proteins, Rep 78, Rep 68, Rep 52 and Rep 40, while the cap reading frame encodes three structural proteins, VP1, VP2 and VP3. The rep reading frame encodes three structural proteins, VP1, VP2 and VP3. The regions, are useful in production of recombinant viral vectors for generations, are useful in production of recombinant viral vectors for generations or antisense delivery vectors. The AAV-1 does not induce the formation of neutralising antibodies specific to any serotype of AAV hence is useful for transforming host cells, and in the preparation of a medicament for the delivery of transgene to a host. The present sequence is a $' ITR of AAV-1 DNA which is useful in the production of recombinant viral vector. The ITR forms a T-shaped hairpin structure
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/note= "Inverted terminal repeat which is capable of
forming T-shaped hairpin structure"
Novel adeno-associated virus serotype 1 polynucleotide useful for preparation of medicament for delivery of a transgene to a host.
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                                                                                                                                                                                                                                                                    Query Match
100.0%; Score 143; DB 3; Length 143;
Best Local Similarity 100.0%; Pred. No. 2.3e-28;
Matches 143; Conservative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                             Sequence 143 BP; 24 A; 50 C; 48 G; 21 T; 0 U; 0 Other;
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119. .226
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'bound moiety= "Rep protein"
[24. .125
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236. .299
/*tag= e
                                                                                                                                                                                                                                                                                                                                                                                                                                GGCAACTCCATCACTAGGGGTAA 143
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Location/Qualifiers
1. .143
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Adeno associated virus serotype 1.
                                  Example 2; Fig 2; 108pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AAD00772 standard; DNA; 4718 BP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      08-SEP-2000 (first entry)
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The invention relates to a novel method for detecting adeno-associated virus (AAV) sequences in a sample, which comprises subjecting a sample containing a DNA to amplification via a polymerase chain reaction (PCR). The AAV sequence have the following activities: cytostatic, antirheumatic, antiarthritic, neuroprotective, antidabetic, antithyroid, dermatological, and antiniflammatory. The ASV sequence can be used in gene therapy or as par of a vaccine to treat disorders. The method is useful in detecting and/or identifying AAV sequences and isolating novel sequences that are identified. The sequences may be used e.g. for preventing or treating hyperproliferative conditions such as cancers and psortaisis, and other autoimmune diseases thy relumatoid arthritis, multiple sclerosis, diabetes, autoimmune thyroiditis, scleroderma or Crohn's disease. This polymucleotide sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     expression construct; adeno-associated virus; integration efficiency element; inverted terminal repeat; integration; chromosome; cancer; lymphome; leukemia; multiple myeloma; neuroblastoma; retinoblastoma; inflammatory disease; arthritis;
                                                                                                                                                                                                                                                                            Detecting adeno-associated virus sequences in a sample, useful for e.g. preventing or treating hyperproliferative or autoimmune diseases, comprises subjecting a sample having a DNA to amplification via
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 4718 BP; 1121 A; 1393 C; 1273 G; 931 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Indela
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 represents an AAV related DNA sequence of the invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             100.0%; Score 143; DB 10;
100.0%; Pred. No. 2.8e-28;
iive 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Adeno-associated virus serotype 1 complete DNA
                                                                                                                                                                                                                                                                                                                                                                                                      Claim 14; SEQ ID NO 6; 419pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           GGCAACTCCATCACTAGGGGTAA 143
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Wilson JM, Alvira M;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ADL13984 standard; DNA; 4718
                   13-NOV-2001; 2001US-0350607P.
17-DEC-22001; 2001US-0341117P.
01-MAY-2002; 2002US-037066F.
05-JUN-2002; 2002US-0386675P.
                                                                                                                                                                                                                                                                                                                                                         polymerase chain reaction.
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                                                                                                                                        (UYPE-) UNIV PENNSYLVANIA.
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                                                                                                                                                                                                                                       WPI; 2003-450984/43.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Local Similarity
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                                                                                                                                                                                       Gao G,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                RESULT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              The present sequence is an adeno-associated virus serotype 1 (AAV-1) DNA characterised by two inverted terminal repeats (ITR) and open reading frames for rep and capaid (Cap) proteins. The rep reading frame encodes four proteins, Rep 78, Rep 68, Rep 52 and Rep 40, while the cap reading frame encodes three structural proteins, VP1, VP2 and VP3. The AAV-1 as equence or its fragments particularly ITRs, rep and cap coding regions, are useful in production of recombinant viral vectors for gene delivery. These vectors can be used as gene therapy vectors, vaccine vectors or antisense delivery vectors. The AAV-1 does not induce the formation of neutralising antibodies specific to any serotype of AAV hence is useful for transforming host cells, and in the preparation of a medicament for the delivery of transgene to a host
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             antirheumatic;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TIGCCCACTCCCTCTCTGCGCGCTCGCTCGGTGGGGCCTGCGGACCAAGGTCCGC
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                                                                                                                                                                                                                P-PSDB; AAY71161, AAY71164, AAY71165, AAY71166, AAY71167, AAY71169
                                                                                                                                                                                                                                                                                                                 a transgene to a host
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         rheumatoid arthritis; multiple sclerosis; diabetes;
autoimmune thyroiditis; scleroderma; Crohn's disease; gene; ds.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 4718 BP; 1121 A; 1393 C; 1273 G; 931 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                      Novel adeno-associated virus serotype 1 polynucleotide useful
preparation of medicament for delivery of a transgene to a hos
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      100.0%; Score 143; DB 3; Length 4718; 100.0%; Pred. No. 2.8e-28;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           adeno-associated virus; AAV; cytostatic; antipsoriatic; ant
antiarthritic; neuroprotective; antidiabetic; antithyroid;
dematological; antinfilammatory; gene therapy; vaccine;
hyperproliferative; cancer; psoriasis; autoimmune disease;
rheumatoid arthritis; multiple sclerosis; diabetes;
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                                                                                                                                                                                                                                                                                                                                                                Claim 1; Fig 1; 108pp; English
                                                 98US-0107114P
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Local Similarity 100.0%;
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  99WO-US025694
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                                                                                              (UYPE-) UNIV PENNSYLVANIA.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Adeno-associated virus 1.
                                                                                                                                                                                            WPI; 2000-376571/32
                                                                                                                                             Xiao W;
  02-NOV-1999;
                                                 05-NOV-1998;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 29-JAN-2004
                                                                                                                                             Wilson JM,
                                                                                                                                                                                                                                           AAY71169.
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Adeno-associated virus 1.
                                      WO2003104392-A2.
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AAF23749/c
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                                                                                                                                                                                                                                                                                      cid sequence encoding an adeno-associated virus innegration efficiency element (AAV INEE), which is devoid of AAV inverted terminal repeats (AAV ITRS) and site-specifically integrates into a host cell chromosome when provided to the host cell in conjunction with an AAV Rep protein. The expression construct can be used as a therapeutic factor for treating a mammal for a pathologic state which is cancer, including lung cancer, colon cancer, renal cancer, and cancer, bile duct cancer, bladder cancer, brain cancer, spinal chord cancer, breast cancer, cancer, broad cancer, esophageal cancer, particular cancer, particular cancer, particular cancer, particular cancer, rethoplostome, skin cancer, stomach cancer, cancer, prostatic cancer, rethoplastoma, swint cancer, particular cancer, thymus cancer or thyroid cancer. Other pathologic state includes inflammatory disease (arthritis), neurodegenerative catset includes inflammatory disease (arthritis), neurodegenerative catset in a particular gene product(8). This sequence corresponds to the AAV serotype I complete DNA including the IEE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  120
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                                                                                                                                                                              New expression construct comprising a nucleic acid sequence encoding an adeno-associated virus integration efficiency element, useful for treating cancer e.g. lung cancer or colon cancer or inflammatory disease
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1 TTGCCCACTCCCTCTCTGCGCGCTCGCTCGCTGGGGGCCTGCGGGACCAAAGGTCCGC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1 TIGCCCACTCCCTCTGCGCGCTCGCTCGGTGGGGCCTGCGGACCAAAGGTCCGC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              parvovirus; rep; cap; DNA binding domain; capsid interacting domain; recombinant hybrid parvovirus particle; recombinant adeno-associated virus; rAAV; AAV; vaccine; gene therapy;
                                                                                                                                                                                                                                                                             The invention relates to an expression construct comprising a nucleic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Length 4718;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match
100.0%; Score 143; DB 10;
Best Local Similarity 100.0%; Pred. No. 2.8e-28;
Matches 143; Conservative 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AAV-1 genomic DNA sequence SEQ ID NO:20.
                                                                                                                                                                                                                                                  Disclosure, SEQ ID NO 3; 62pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                GGCAACTCCATCACTAGGGGTAA 143
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                                                                                                                       Philpott N;
                                                                                             CORR ) CORNELL RES FOUND INC.
                                                                  09-APR-2002; 2002US-0371044P.
                                     09-APR-2003; 2003WO-US011191.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          11-MAR-2004 (first entry)
                                                                                                                                                   WPI; 2003-833723/77.
                                                                                                                       Falck-Pedersen ES,
                                                                                                                                                                                                                     e.g. arthritis
           23-OCT-2003
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       gene, da.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                sequence.
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The present invention describes a polymucleotide (I), comprising

C rep coding sequences and parvovirus cap coding sequences. The

C rep coding sequences encodes a DNA binding domain from a first

parvovirus, and a capsid interacting domain from a parvovirus different

C parvovirus, and a capsid interacting domain from a parvovirus different

C from the different parvovirus. Also described: (1) a vector comprising

(I); (2) a cell comprising (I), or parvovirus esp coding sequences and

CC parvovirus cap coding sequences. Where the rep coding sequences and

DNA binding domain from a first parvovirus and a capsid interacting

CC domain from a parvovirus different from the different parvovirus, and

CC domain from a parvovirus different from the different parvovirus, and

CC coding sequences comprise sequences from the different parvovirus, and

CC coding sequences are stably integrated into the genome of the

CC coding sequences are stably integrated into the genome of the

CC coding sequences are stably integrated into waccines, and in

CC associated vitus (rAAV) particle. (I) can be used in producing higher

CC cll; and lybrid parvoviruses or parvovirus vectors, which may be used in

CC ameliorate the symptoms associated with any disorder related to gene

CC ameliorate the symptoms associated with any disorder related to gene

CC active and inverse of invisor or in diagnostic and sereening

CC methods. The present sequence is used in the exemplification of the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1 THECCCACTCCCTCTCTGCGCGCTCGCTCGGTCGGTGGGCCTGCGGACCAAAGGTCCGC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         New polynucleotides comprising parvovirus rep coding sequences and parvovirus cap coding sequences, useful in producing higher stocks of hybrid parvovirus vectors for delivering therapeutic nucleic acids to
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 4718 BP; 1121 A; 1393 C; 1273 G; 931 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Disclosure; SEQ ID NO 20; 115pp; English
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                                                                                                                                                                             18-DEC-2001; 2001US-0341919P.
                                                                                    02-DEC-2002; 2002WO-US038423
                                                                                                                                                                                                                                                                                                                                                           Rabinowitz JE;
                                                                                                                                                                                                                                                                       (UYNC-) UNIV NORTH CAROLINA
                                                                                                                                                                                                                                                                                                                                                                                                                                                    WPI; 2004-062324/06.
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                                                                                                                                                                                                                                                                                                                                                           Samulski RJ,
18-DEC-2003
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acid sequence encoding an adeno-associated virus integration efficiency element (AAV IEB), which is devoid of AAV inverted terminal repeats (AAV INVERDED of the AAV INVERTED of the AAV INVERDED OF THE AAVING OF
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 New expression construct comprising a nucleic acid sequence encoding an adeno-associated virus integration efficiency element, useful for treating cancer e.g. lung cancer or colon cancer or inflammatory disease
chromosome, cancer; lymphoma; leukemia; multiple myeloma; neuroblastoma;
retinoblastoma; inflammatory disease; arthritis;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1 TIGCCCACTCCCTCTCTGCGCGCTCGCTCGGTGGGGCCTGCGGACCAAAGGTCCGC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         invention relates to an expression construct comprising a nucleic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             97.1%; Score 138.8; DB 10; Length
98.6%; Pred. No. 3.5e-27;
ive 0; Mismatches 2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Disclosure; SEQ ID NO 2; 62pp; English.
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                                                                                                                                                                                                                                                                                                                                                                                                                     Philpott N;
                                                                                                                                                                                                                                                                                                                                                                    (CORR ) CORNELL RES FOUND INC.
                                                                                                                                                                                                                                                                                                                 09-APR-2002; 2002US-0371044P.
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                                                                                                                                                                                                                                                                 09-APR-2003; 2003WO-US011191
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                                                        neurodegenerative disease.
                                                                                                        Adeno-associated virus 6.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                     WPI; 2003-833723/77
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                                                                                                                                                                                                                                                                                                                                                                                                                       Falck-Pedersen ES,
                                                                                                                                                           WO2003087334-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      e.g. arthritis.
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                                                                                                                                                                                                           23-OCT-2003
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ADG39763/c
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        2 X X X E
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               The present invention relates to adeno-associated virus serotypes. The present sequence is the DNA sequence of one such serotype (AAV6). AAV6 can be used to contruct AAV viral vectors for use in gene therapy for a range of disorders: cystic fibrosis, cancer, AIDS, atherosclarosis, sickle cell anaemia, thalassaemia, blood clotting disorders and diabetes. The AAV viral vectors have increased transduction efficiency of a particular host cell as the AAV viron containing the AAV vector genome can be modified to express a capsid protein of an AAV serotype that transduces the selected host cell
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expression construct; adeno-associated virus;
integration efficiency element; inverted terminal repeat; integration;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Adeno-associated virus serotype 6 and viral vector derived from it for gene therapy of cystic fibrosis, cancer, acquired immunodeficiency syndrome, sickle cell anemia, thalassemia and diabetes.
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                                                                                                                                   AAV6; gene therapy; AAV viral vector; cystic fibrosis; cancer; AIDS; atherosclerosis; sickle cell anaemia; thalassaemia; blood clotting disorder; diabetes; ss.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         97.1%; Score 138.8; DB 4; Length 4683; 98.6%; Pred. No. 3.5e-27; ive 0; Mismatches 2; Indels 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 4683 BP; 1114 A; 1363 C; 1277 G; 929 T; 0 U; 0 Other;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Claim 1; Fig 1; 50pp; English
                                                                                                                                                                                                                                                                                                                                                                                                  97US-00873168
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                                     (first entry)
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                                                                                                                                                                                                                                         Adeno associated virus.
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Matches 140; Conserv
                                                                                     AAV6 DNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                  11-JUN-1997;
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                                     28-MAR-2001
                                                                                                                                                                                                                                                                                               US6156303-A.
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ADE76502 standard; DNA; 4721

RESULT 9 ADE76502

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The present invention describes a polynucleotide (1), comprising parvovirus rep coding sequences and parvovirus cap coding sequences and parvovirus cap coding sequences encodes a DNA binding domain from a first parvovirus, and a capsid interacting domain from a parvovirus different parvovirus. The cap coding sequence comprising (1); or parvovirus comprising (1); or parvovirus rep coding sequences and parvovirus and capsid interacting constition a parvovirus different parvovirus and a capsid interacting domain from a parvovirus and a capsid interacting domain from a parvovirus and a capsid interacting coding sequences are stably integrated into the genome of the coding sequences are stably integrated into the genome of the cell; and (3) producing a recombinant hybrid parvovirus particle or adenocastic divirus (rAAV) particle. (1) can be used in producing higher stocks of hybrid parvoviruses or parvovirus vectors, which may be used in the delivery of nucleic acids having biological effect to treat or amplicate the symptoms associated with any disorder related to gene expression. The polynucleotide may be used to produce a parvovirus vector companies in subject, e.g. for vaccination. The parvovirus vector may also be used to produce a parvovirus vector may also be used to produce an antisense nucleic acid to a cell in vitro or in vivo, or in diagnostic and screening methods. The present sequence is used in the exemplification of the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         New polynucleotides comprising parvovirus rep coding sequences and parvovirus cap coding sequences, useful in producing higher stocks of hybrid parvovirus vectors for delivering therapeutic nucleic acids to a subject.
                                                          parvovirus; rep; cap; DNA binding domain; capsid interacting domain; recombinant hybrid parvovirus particle; recombinant adeno-associated virus; rAAV; AAV; vaccine; gene therapy;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Disclosure, SEQ ID NO 25; 115pp; English.
                      AAV-6 genomic DNA sequence SEQ ID NO:25.
                                                                                                                                                                                                                                                                                                                                               18-DEC-2001; 2001US-0341919P
                                                                                                                                                                                                                                                                                                    02-DEC-2002; 2002WO-US038423
                                                                                                                                                                                                                                                                                                                                                                                       (UYNC-) UNIV NORTH CAROLINA.
                                                                                                                                                                                                                                                                                                                                                                                                                                  Rabinowitz JE;
                                                                                                                                                                       Adeno-associated virus 6.
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                                                                                                                                                    4683 TTGCCCACTCCCTCTATGCGCGCTCGCTCGGTGGGGCCTGCGGACCAAAGGTCCGC
                                                                                                                                                                                          TTGCCCACTCCCTCTCTGCGCGCTCGCTCGCTCGGTGGGGCCTGCGGACCAAAGGTCCGC
                                                                          0; Gaps
                                97.1%; Score 138.8; DB 12; Length 4683; 98.6%; Pred. No. 3.5e-27; ive 0; Mismatches 2; Indels 0;
Sequence 4683 BP; 1114 A; 1363 C; 1277 G; 929 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                              GOCAACTCCATCACTAGGGGTA 4542
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                              Query Match
Best Local Similarity 98.6'
Matches 140; Conservative
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The invention relates to a novel method for detecting adeno-associated virus (AAV) sequences in a sample, which comprises subjecting a sample containing a DNA to amplification via a polymerase chain reaction (PCR). The AAV sequence have the following activities: cytostatic, antithered antithered dematic, antiarthritic, neuroprotective, antidiabetic, antithyroid, dermatological, and antiinflammatory. The AAV sequence can be used in gene therapy or as part of a vaccine to treat disorders. The method is useful in detecting and/or identifying AAV sequences and isolating novel sequences that are identified. The sequences may be used e.g. for preventing or treating hyperproliferative conditions such as cancers and psoriasis and other autoimmune diseases like rheumatoid arthritis, multiple sclerosis, diabetes, autoimmune thyroiditis, scleroderma or Crohn's disease. This polymucleotide sequence represents an AAV related DNA sequence of the invention.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Detecting adeno-associated virus sequences in a sample, useful for e.g. preventing or treating hyperproliferative or autoimmune diseases, comprises subjecting a sample having a DNA to amplification via
                                                                                                                                     adeno-associated virus, AAV; cytostatic; antipsoriatic; antirheumatic; antiarthritic; neuroprotective; antidiabetic; antithyroid;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1 TTGGCCACTCCCTCTATGCGCGCTCGCTCGCTCGGCCTGCGGGCCTGCGGAAGGTCCGC
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                                                                                                                                                                          dermatological; antiînflammatory; gene therapy; vaccîne; hyperproliferative; cancer; psoriasis; autoimmune disease; rheumatoid arthritis; multiple sclerosis; disbetes; autoimmune thyroiditis; scleroderma; crohn's disease; gene;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            4; Indels
                                                                                               Adeno-associated virus (AAV) related DNA, SEQ ID No 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            0; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                    12-NOV-2002; 2002EP-00257826.
                                                                                                                                                                                                                                                                                                                                                                                                                                        13-NOV-2001; 2001US-0350607P.
17-DEC-2001; 2001US-0341117P.
01-MAY-2002; 2002US-0377066P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gao G, Wilson JM, Alvira M;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      05-JUN-2002; 2002US-0386675P
                                                        (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             (UYPE-) UNIV PENNSYLVANIA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             polymerase chain reaction.
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Matches 138; Conservative
                                                                                                                                                                                                                                                                              Adeno-associated virus 7.
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                                                        29-JAN-2004
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                                                                                                                                                                                                                                                                                                                                                           14-MAY-2003.
                  ADE76502;
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Matches 138; Conservative
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parvovirus rep coding sequences and parvovirus cap coding sequences. The
rep coding sequences encodes a DNA binding domain from a first
parvovirus, and a capsid interacting domain from a parvovirus different
from the first parvovirus. The cap coding sequence comprises sequences
from the different parvovirus. Also described: (I) a vector comprising
(I); (2) a cell comprising (I), or parvovirus rep coding sequences and
parvovirus cap coding sequences, where the rep coding sequences encode a
coding sequences comprise sequences from the different parvovirus, the cap
coding sequences are stably integrated into the genome of the
cell; and (3) producing a recombinant hybrid parvovirus particle or adeno
associated virus (rAAV) particle. (I) can be used in vaccines, and in
gene therapy. The polynucleotide (I) can be used in vaccines, and in
gene therapy of nucleic acids having biological effect to treat or
central symptoms associated with any disorder related to gene or
annellorate the symptoms associated with any disorder related to gene
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               expression. The polymuclectide may be used to produce a parvovirus vector to express an immunogenic polypeptide in a subject, e.g. for vaccination. The parvovirus vector may also be used to provide an antisense nucleic acid to a cell in vitro or in vivo, or in diagnostic and screening methods. The present sequence is used in the exemplification of the
 New polynuclectides comprising parvovirus rep coding sequences and parvovirus cap coding sequences, useful in producing higher stocks of hybrid parvovirus vectors for delivering therapeutic nucleic acids to a
                                                                                                                                                                                                                                                                                                                          parvovirus; rep; cap; DNA binding domain; capsid interacting domain; recombinant hybrid parvovirus particle; recombinant adeno-associated virus; rAAV; AAV; vaccine; gene therapy;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 4721 BP; 1108 A; 1405 C; 1301 G; 907 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Disclosure; SEQ ID NO 26; 115pp; English.
                                                                                                                                                                                                                                                                                      AAV-7 genomic DNA sequence SEQ ID NO:26.
                                         GGCAACTCCATCACTAGGGGTA 142
                                                           ADG39764 standard; DNA; 4721 BP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                18-DEC-2001; 2001US-0341919P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          02-DEC-2002; 2002WO-US038423.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Samulski RJ, Rabinowitz JE;
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                                                                                                                                                                                                                                                    (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                           Adeno-associated virus 7.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                WPI; 2004-062324/06.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      present invention
                                                                                                                                                                                                                                                                                                                                                                                                                                                               WO2003104392-A2
                                                                                                                                                                                                                                                  11-MAR-2004
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       18-DEC-2003
                                                                                                                                                                                                                ADG39764;
                                                                                                                                                                                                                                                                                                                                                                                         gene; da.
                                       121
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                                                                                                                                       RESULT 10
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94.8%; Score 135.6; DB 12; Length 4721;

Query Match

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       The specification describes a method for lowering total cholesterol levels in a subject. The method comprises delivering to the subject a recombinant adeno-associated virus (AAV) comprising a gene encoding a
                                              1 TTGGCCACTCCTCTATGCGCGCTCGCTCGCTCGGTGGGCCTGCGGAAGGTCGGC
                                1 TTGCCCACTCCCTCTCTGCGCGCTCGCTCGGTGGGGCCCTGCGGACCAAAGGTCCGC
                                                                                                                                                                                                                                                                                                             antiarteriosclerotic; antilipemic; gene therapy; cholesterol; apolipoprotein E; apoE; apolipoprotein A; apoA; atherosclerosis; lipoprotein defect; ss.
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0
          4; Indels
Pred. No. 2.5e-26;
0; Mismatches 4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Disclosure; SEQ ID NO 7; 69pp; English.
                                                                                                                                                                                                                                                                                          Nucleotide sequence of AAV serotype 7.
                                                                                                                                                                                                                                                                                                                                                                                                                                                    /*tag= b
/note= "encodes vpl"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          *tag= c
note= "encodes vp2"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /note= "encodes vp3"
4704. .4721
                                                                                                                                121 GGCAACTCCATCACTAGGGGTA 142
                                                                                                                                               121 GCCAACTCCATCACTAGGGGTA 142
                                                                                                                                                                                                                                                                                                                                                                                         Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                  1. .107
/*tag= a
/note= "5' ITR"
                                                                                                                                                                                                                  ADV67509 standard; DNA; 4721 BP
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/note= "3' ITR"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1234. .3049
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                                                                                                                                                                                                                                                                  (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            *tag=
                                                                                                                                                                                                                                                                                                                                                                 Adeno-associated virus.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Wilson JM;
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772/c
AAD00772 standard; DNA; 4718
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270. .275
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                                                                                                                                                                        Matches 138; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               .143
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               vaccine, transgene, ss.
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                                                                                                                                                           Local Similarity
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AAD00772/c
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human apolipoprotein E (apoE) or apoA under the control of a regulatory control sequence which directs expression of the gene. The recombinant AAV also comprises a capsid protein selected from an AAV serotype (e.g. AAV) or AAVB) which preferentially expressingh levels of transgene in live. A therapeutically effective amount of apoE or apoA expression is obtained upon delivery of low dose of AAV. The method of the invention is useful for lowering total cholesterol levels in a subject, e.g. for treating atherosclerosis, and for correcting defects in lipoprotein. The present sequence represents AAV serotype 7 (AAV7), which may be used to produce recombinant AAV vectors of the invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      The invention relates to an adeno-associated virus (AAV) clade comprising at least three AAV members, where each member of the AAV clade is
                                                                                                                                                                                                                                                                               1 TYGGCCACTCCTCTATGCGCGCTCGCTCGGTGGGGCCTGCGGACCAAAGGTCCGC 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            rheumatoid arthritis; multiple sclerosis; sarcoidosis; diabetes; scleroderma; psoriasis; vascultis; Crohm's disease; hemophilia; HIV; bacterial infection; cancer; ulcerative colitis; antirheumatic; antiarthritic; neuroprotective; antiplammatory; antidiabetic; antipporiatic; vasotropic; gastroincestinal-gen.; hemostatic; anti-HIV; virucide; antibacterial; cytostatic; antiulcer; dermatological; ds.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            New adeno-associated virus (AAV) clade comprising at least three AAV members, useful for preventing and/or treating arthritis, multiple sclerosis, diabetes, scleroderma, psoriasis, hemophilia, HIV, bacterial
                                                                                                                                                                                                                           1 TIGCCCACTCCCTCTCTGCGCGCTCGCTCGCTCGGGGGCCTGCGGACCAAAGGTCCGC
                                                                                                                                                                                                   Gaps
                                                                                                                                                                     Query Match

94.8%; Score 135.6; DB 14; Length 4721;

Best Local Similarity 97.2%; Pred. No. 2.5e-26;

Matches 138; Conservative 0; Mismatches 4; Indels 0;
                                                                                                                                               Sequence 4721 BP; 1108 A; 1405 C; 1301 G; 907 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Vandenberghe LH;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Adeno-associated virus DNA SEQ ID NO 180.
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                                                                                                                                                                                                                                                                                                                                 GGCAACTCCATCACTAGGGGTA 142
                                                                                                                                                                                                                                                                                                                                                        GCCAACTCCATCACTAGGGGTA 142
                                                                                                                                                                                                                                                                                                                                                                                                                         ADZ27030 standard; DNA; 4721 BP
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29-APR-2004; 2004US-0566546P.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                             (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Adeno-associated virus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      infection and cancer.
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phylogenetically related as determined using a Neighbor-Joining heuristic by a bootstrap value of at least 75 % per 100 isolates and a Poisson correction distance measurement of no more than 0.05. The methods and compositions of the present invention are useful for the prevention and/or treatment of rheumatoid arthritis, multiple sclerosis, and/or treatment of compositions, psorialsis, wasculitis, Crohn's disease, hemophilia, HIV, bacterial infection, cancer and ulcerative collits. The present sequence represents an adeno-associated virus DNA.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1 TIGCCCACTCCCTCTGCGCGCTCGCTCGCTCGGTGGGGCCTGCGGACCAAAGGTCCGC
                                                                                                                                                                                                                                                                                                                                                            Gaps
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                                                                                                                                                                                                                                                                                                    94.8%; Score 135.6; DB 14; Length 4721; 97.2%; Pred. No. 2.5e-26; cive 0; Mismatches 4; Indels 0;
                                                                                                                                                                                                                                                  Sequence 4721 BP; 1108 A; 1405 C; 1301 G; 907 T; 0 U; 0 Other;
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/note= "Terminal resolute site (TRS)"
219. .226
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'bound moiety= "Rep protein"
[24. .125
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label= P5_promoter
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               GGCAACTCCATCACTAGGGGTA 142
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335. .2272
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/note= "E box"
236. .299
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The present sequence is an adeno-associated virus serotype 1 (AAV-1) DNA characterised by two inverted terminal repeats (ITR) and open reading frames for rep and capsid (cap) proteins. The rep reading frame encodes four proteins, Rep 78 Rep 68, Rep 52 and Rep 40, while the cap reading frame encodes three structural proteins, VP1, VP2 and VP3. The AAV-1 sequence or its fragments particularly ITRs, rep and cap coding regions, are useful in production of recombinant viral vectors for gene delivery. These vectors can be used as gene therapy vectors, vaccine vectors or antisense delivery vectors. The AAV-1 does not induce the formation of neutralising antibodies specific to any serotype of AAV hence is useful for transforming host cells, and in the preparation of a medicament for the delivery of transgene to a host.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 antirheumatic;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                               4718 TIGCCCACTCCCTCTGCGCGCTCGCTCGCTCGGTGGGGCCGGCAGAGCAGAGCTCGC
          Novel adeno-associated virus serotype 1 polynucleotide useful for preparation of medicament for delivery of a transgene to a host.
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                                                                                                                                                                                                                                                                                                                                                              Query Match

83.2%; Score 119; DB 3; Length 4718;
Best Local Similarity 89.5%; Pred. No. 5.8e-22;
Matches 128; Conservative 0; Mismatches 15; Indels
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antiarthritic; neuroprotective; antidiabetic; antithyroid;
dermatological; antiinflammatory; gene therapy; vaccine;
hyperproliferative; cancer; psoriasis; autoimmune disease;
rheumatoid arthritis; multiple sclerosis; diabetes;
autoimmune thyroiditis; scleroderma; Crohn's disease; gene;
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                                                                   Claim 1; Fig 1; 108pp; English.
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17-DEC-2001; 2001US-0341117P.
01-MAY-2002; 2002US-0377066P.
05-JUN-2002; 2002US-0386675P.
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                               /function= "regulates replication and integration of AAV DNA into host cell's chromosome" /note= "The coding region is interrupted by intron"
                                                                                                                                                                                                                                                                                                                                   function= "regulates replication and integration of AAV ONA into host cell's chromosome"
                                                                                                                                                                                                                                                                                                                                                                                                                                         /Function= "regulates replication and integration of AAV onA into host cell's chromosome"
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P-BSDB; AAY71161, AAY71164, AAY71165, AAY71166, AAY71167, AAY71168,
AAY71169.
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note= "P40 RNA"
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4659

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New expression construct comprising a nucleic acid sequence encoding an adeno-associated virus integration efficiency element, useful for treating cancer e.g. lung cancer or colon cancer or inflammatory disease

Disclosure, SEQ ID NO 3; 62pp; English

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4718 TTGCCCACTCCCTCTCTGCGCGCTCGCTCGCTCGGTGGGGCCGGCAGAGCAGAGCTCTGC 4659
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     The invention relates to a novel method for detecting adeno-associated virus (AAV) sequences in a sample, which comprises subjecting a sample containing a DNA to amplification via a polymerase chain reaction (PCR). The AAV sequence have the following activities: cytostatic, antirheumatic, antiarthritic, neuroprotective, antidabetic, antirhyroid, dermatological, and antiinflammatory. The AAV sequence can be used in gene therapy or as part of a vaccine to treat disorders. The method is useful in detecting and/or identifying AAV sequences and isolating novel sequences that are identified. The sequences may be used e.g. for preventing or treating hyperproliferative conditions such as cancers and psoriasis, and other autoimmune diseases like rheumatoid arthritis, multiple sclerosis, diabetes, autoimmune thyroiditis, scleroderma or Crohn's disease. This polynucleotide sequence
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              Detecting adeno-associated virus sequences in a sample, useful for preventing or treating hyperproliferative or autoimmune diseases, comprises subjecting a sample having a DNA to amplification via
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89.5%; Pred. No. 5.8e-22;
tive 0; Mismatches 15
                                                                                                  Claim 14; SEQ ID NO 6; 419pp; English.
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The invention relates to an expression construct comprising a nucleic acid sequence encoding an adeno-associated virus integration efficiency element (AAV IEEE), which is devoid of AAV inverted terminal repeats (AAV ITER) and stre-specifically integrates into a host cell chromosome when provided to the host cell in conjunction with an AAV Rep protein. The provided to the host cell in conjunction with an AAV Rep protein. The conjunction with an AAV Rep protein. The mammal for a pathologic state which is cancer, including lung cancer, colon cancer, renal cancer, anal cancer, bile duct cancer, bladder cancer, lymphoma, endomeral cancer, beast cancer, carcer, multiple myeloma, neuroblastoma, ovarian cancer, prostatic cancer, retinoblastoma, skin cancer, stomach cancer, cancer, multiple myeloma, neuroblastoma, ovarian cancer, prostatic cancer, thymus cancer thyroid cancer, other pathologic state includes inflammatory disease (arthritis), neurodegenerative disease, a disease of an organ attributed to the presence of increased or decreased level of a particular gene product(8). This sequence

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Pred. No. 5.8e-22;
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Search completed: November 28, 2005, 19:55:37

Job time : 69.9124 secs

chromosome; cancer; lymphoma; leukemia; multiple myeloma; neuroblastoma; retinoblastoma; inflammatory disease; arthritis; expression construct; adeno-associated virus; integration efficiency element; inverted terminal repeat; integration;

neurodegenerative disease.

Adeno-associated virus 1.

WO2003087334-A2. 23-OCT-2003 Philpott N;

Falck-Pedersen ES,

(CORR) CORNELL RES FOUND INC. 09-APR-2002; 2002US-0371044P. 09-APR-2003; 2003WO-US011191

88; cytostatic; neuroprotective; antiinflammatory; gene therapy;

Adeno-associated virus serotype 1 complete DNA

c 23 34.4 24.1 745 2 BG837739 BG837739 Call AG127787 Pan trogl 24 34.2 23.9 364 5 BY014749 BY018719 BY018719 BY018719 BY018719 BY018719 BY018719 BY018719 BY018719 <th>RESULT 1 BG490707/c LOCUS BG490707/c LOCUS BG490707 BG490707 BG490707 ACCESSION RRNA Sequence. ACCESSION BG490707.1 GI:13452217 RRNA Sequence. ACCESSION BG490707.1 GI:13452217 KENTION BG490707.1 GI:13452217 BG490707.1 GI:13452217 KENTON BG490707.1 GI:13452217 BG490707.1 GI:13452217 KENTON BG490707.1 GI:13452217 BG49070707.1 GI:13452217 BG490707.1 GI:13452217 BG490707.1 GI:13452217 BG490707.1 GI:13452217 BG490707.1 GI:13452217 BG490707.1 GI:13452217 BG490707.1 GI:13452017 BG490707.1 GI:13452017 BG49070707 BG490707 BG490707 BG4907 BG4907</th> <th>DNA Sequencing by: Incyte Genomics, Inc. Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at: http://lmage.llnl.gov Plate: LLCM1401 row: e column: 04 High quality sequence stop: 182. Location/Qualifiers Location/Qualifiers I. 0.6 / organism="Homo sapiens" //mol_type="mRNA" //db_ref="mRNA" //db_ref="raxon:9606" //clone="INAME:4638699" //tissue_type="large cell carcinoma" //lab.bost="Bl108" //lab.bost="Bl108" //lab.bost="Bl108" //clone lb.eft" //clone lb.eft"</th>	RESULT 1 BG490707/c LOCUS BG490707/c LOCUS BG490707 BG490707 BG490707 ACCESSION RRNA Sequence. ACCESSION BG490707.1 GI:13452217 RRNA Sequence. ACCESSION BG490707.1 GI:13452217 KENTION BG490707.1 GI:13452217 BG490707.1 GI:13452217 KENTON BG490707.1 GI:13452217 BG490707.1 GI:13452217 KENTON BG490707.1 GI:13452217 BG49070707.1 GI:13452217 BG490707.1 GI:13452217 BG490707.1 GI:13452217 BG490707.1 GI:13452217 BG490707.1 GI:13452217 BG490707.1 GI:13452217 BG490707.1 GI:13452017 BG490707.1 GI:13452017 BG49070707 BG490707 BG490707 BG4907 BG4907	DNA Sequencing by: Incyte Genomics, Inc. Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at: http://lmage.llnl.gov Plate: LLCM1401 row: e column: 04 High quality sequence stop: 182. Location/Qualifiers Location/Qualifiers I. 0.6 / organism="Homo sapiens" //mol_type="mRNA" //db_ref="mRNA" //db_ref="raxon:9606" //clone="INAME:4638699" //tissue_type="large cell carcinoma" //lab.bost="Bl108" //lab.bost="Bl108" //lab.bost="Bl108" //clone lb.eft"
GenCore version 5.1.6 Copyright (c) 1993 - 2005 Compugen Ltd. OM nucleic - nucleic search, using sw model Run on: November 28, 2005, 18:24:29; Search time 454.049 Seconds (without alignments) 14735.325 Million cell updates/sec Title: US-10-696-900-1_COPY_1_143 Sequence: 1 ttgcccactccctctctgcgaactccatcactaggggtaa 143 Scoring table: Scoring table: Capop 10.0, Gapext 1.0 Searched: 41078325 seqs, 23393541228 residues Total number of hits satisfying chosen parameters: Minimum DB seq length: Oncompose	bcessing: Minimu Maximu Listing Maximu Listing	38.2 26.7 763 2 BG499707 37.8 26.4 1021 5 BUB3899 36.2 25.3 920 2 BG76456 36.2 25.3 1021 5 BUB38990 35.8 25.0 604 3 BI531460 35.8 25.0 1074 10 CL507458 35.6 24.9 860 2 BF51862 35.4 24.8 860 2 BF57862 35.4 24.8 860 2 BF57862 35.4 24.8 1123 10 AG01476 35.2 24.6 1123 10 AG074763 35.2 24.6 1023 10 CL751558 35 24.5 844 10 CL751558 34.8 24.3 926 8 CV775269 34.6 24.2 637 7 CN038418 34.6 24.2 2088 10 CL507788 34.6 24.2 2088 10 CL507788

Query Match

ORIGIN

Best Loc Matches

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Email: genome-ree@gac.riken.jp, URL:http://genome.gac.riken.jp/
Carninci,P., Shibata,Y., Hayatsu,N., Sugahara,Y., Shibata,K.,
Itoh,M., Konno,H., Okazaki,Y., Muramatau,M. and Hayashizaki,Y.
Normalization and subtraction of cap-trapper-selected cDNAs to
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Kondo,S., Shinaqawa, S., Hara,A., Itoh,M., Kawai,J., Shibata,K. and
                                                                                                                                                                                                                                                                                                                                                                                                                                                   Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi, Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Euteleostomi, Sciurognath; Muroidea; Muridae; Murinae; Mus.

E. 1 (bases 1 to 644)
S. Arakawa, T., Carninci, P., Fukuda, S., Furuno, M., Hanagaki, T., Hara, A., Hiramoto, K., Hori, F., 18hii, Y., Ito, M., Kawai, J., Konno, H., Kouda, M., Koya, S., Matsuyama, T., Miyazaki, A., Nomura, K., Ohno, M., Okazaki, Y., Okido, T., Salto, R., Sakai, C., Sakai, K., Sano, H., Sasaki, D., Shibata, K., Shinagawa, A., Takahashi, T., Sogabe, Y., Suzuki, H., Tagawa, M., Takahashi, F., Takeda, Y., Tanaka, T., Toya, T., Muramatsu, M. and Hayashizaki, Y. RIKEN Mouse ESTS (Arakawa, T., et al. 2001)
L Unpublished (2001)
                                                                                                                                                                                                                                         EST 26-OCT-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Laboratory for Genome Exploration Research Group, RIKEN Genomic Sciences Center(GSC), Yokohama Institute
The Institute of Physical and Chemical Research (RIKEN)
1-7-22 Subehiro-cho, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan Tel: 81-45-503-9216
Fax: 81-45-503-9216
Email: genome-res@gsc.riken.jp, URL:http://genome.gsc.riken.in/
644 bp mRNA linear EST 26-OCT-20
BB633576 RIKEN full-length enriched, adult male hypothalamus Mus
musculus cDNA clone A230067E15 5', mRNA sequence.
BB632576
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Hayablizaki,Y.

Computational Analysis of Full-Length Mouse cDNAs Compared with Human Genome Sequences. Mamm. Genome. 12, 673-677 (2001)

Please visit our web site (http://genome.gsc.riken.go.jp) for further details.
                                                    70 AGCTCTGCTCTGCCGGCCCCCACCGAGCGAGCGAGCGCGCAGAGAGGGAGTGGG 122
                                                                                   tissue type="hypothalamus"
/dev stage="adult"
/lab_host="DH108"
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/organism="Mus musculus"
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/db_xref="taxon:10090"
/clone="A230067E15"
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                                                                                                                                                                                       201 AGGCTACGCCTTCGCGGGCCTGACGCGGGGGGGGGGCTGGTGCCGGCGTGCCGGGCT
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Individae, Homo.

Individae, Homo.

Independent to 1021)

National Institutes of Health, Mammalian Gene Collection (MGC)

National Institutes of Health, Mammalian Gene Collection (MGC)

Unpublished (1999)

Contact: Robert Strausberg, Ph.D.

Contact: Robert Straushorp

Contact: Robert Straushorp

CDNA Library Preparation: Whin Laboratory

CDNA Library Preparation: Well M.A.G.E. Consortium (LLNL)

DNA Sequencing by: Agencourt Bioscience Corporation

Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at:

http://mage.llnl.gov

Plate: LLCM2413 row: p column: 02

High quality sequence start: 36

Location/Qualifiers
                                                                                                                                                                                                                                                                  68 AGAGCTCTGCTCTGCCGGCCCCACCGAGCGAGCGAGCGCGCCAGAGAGGAAGTGGGCAACT 127
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Mammalia, Eutheria, Euarchontoglires, Primates, Catarrhini,
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                                            Score 38.2; DB 2; Length 763;
Pred. No. 10;
                                                                                                         Indels
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                                                                                                         53;
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                                                                                                      0; Mismatches
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                                               26.7%;
56.9%;
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                                                                          Local Similarity 56.9 tes 70; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Homo sapiens
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Best Local S:
Matches 66
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VERSION KEYWORDS SOURCE ORGANISM

ACCESSION

TITLE JOURNAL COMMENT REFERENCE AUTHORS

FEATURES

ORIGIN

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BU838990/c DEFINITION

RESULT 2

셤 ò 8

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Gaps

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into BcoRI/XhoI sites using the following 5' adaptor: GGCACGAG(G). Size-selected >500bp for average insert size 1.8kb. Library constructed by Ling Hong in the laboratory of Gerald M. Rubin (University of California, Berkeley) using ZAP-CDNA synthesis kit (Stratagene) and Superscript II. RT (Life Technologies). Note: this is a NIH_MGC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  602 égécifogacadagérrandágirégrégrégégécénandon est segérranda est est 661
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       80 TGCCGGCCCCACCGAGCGAGCGCGCGCAGAGGGAGTGGGCAACTCCATCACTAGGG 139
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                                                                                                                                                                                                                                                                                                   Score 36.2; DB 2; Length 920;
Pred. No. 34;
0; Mismatches 53; Indels (
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                                                                                                                                                                                                            Library. |"
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CNS0072Q
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KEYWORDS
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                                                                                                                                                                                                                                                                                                                        /Lisaue_type="malanotic melanoma, high MDR (cell line)"
/lab host="DH10B (phage-resistant)"
/clone lib="NTH MGC 49"
/note="Organ: Skin; Vector: pOTB7; Site 1: XhoI; Site 2:
EcoRI; cDNA made by oligo-dT priming. Directionally cloned
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              920 bp mRNA linear EST 15-WAY-2001 602736258F1 NIH MGC_49 Homo sapiens cDNA clone IMAGE:4861407 5', BG764368
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ô
                                                                 Incremistre 1: Sall; Site_2: BamHI; cDNA library was prepared and sequenced in Mouse Genome Encyclopedia Project of Genome Exploration Research Group in Riken Genomic Sciences Center and Genome Science Laboratory in RIKEN. Division of Experimental Animal Research in Riken contributed to prepare mouse tissues. 1st strand cDNA was gandadadadadadadaccandagaccandagaccandagaccantriptricandagaccandagaccandagaccantriptricandagaccandagaccantriptricandagaccandagaccantricandagaccandagaccantricandagaccandagaccantricandagaccandagaccantricandagaccandagaccantricandagaccandagaccantricandagaccandagaccantricandagaccandagaccantricandagaccandagaccandagaccantricandagaccandagaccandagaccantricandagaccandagaccantricandagaccandagaccandagaccandagaccantricandagaccandagaccandagaccandagaccantricandagaccandagaccandagaccandagaccantricandagaccandagaccandagaccandagaccandagaccantricandagaccandagaccandagaccantricandagaccandagaccandagaccantricandagaccandagaccandagaccantricandagaccandagaccandagaccandagaccantricandagaccandagaccandagaccandagaccandagaccandagaccandagaccandagaccandagaccandagaccandagaccandagaccandagaccandagaccandagaccandagaccandagaccandagaccandagaccandagaccandagaccandagaccandagaccandagaccandagaccandagaccandagaccandagaccandagaccandagaccandagaccandagaccandagaccandagaccandagaccandagaccandagaccandagaccandagaccandagaccandagaccandagaccandagaccandagaccandagaccandagaccandagaccandagaccandagaccandagaccandagaccandagaccandagaccandagaccandagaccandagaccandagaccandagaccandagaccandagaccandagaccandagaccandagaccandagaccandagaccandagaccandagaccandagaccandagaccandagaccandagaccandagaccandagaccandagaccandagaccandagaccandagaccandagaccandagaccandagaccandagaccandagaccandagaccandagaccandagaccandagaccandagaccandagaccandagaccandagaccandagaccandagaccandagaccandagaccandagaccandagaccandagaccandagaccandagaccandagaccandagaccandagaccandagaccandagaccandagaccandagaccandagaccandagaccandagaccandagaccandagaccandagaccandagaccandagaccandagaccandagaccandagaccandagaccandagaccandagaccandagaccandagaccandagaccandagaccandagaccandagaccandagaccandagaccandagaccandagaccandagaccandagacc
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     11 CCTCTCTGCGCGCTCGCTCGCTCGGTGGGGCCTGCGGACCAAAGGTCCGCAGACGCCGGA 70
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Euarchontoglires, Primates, Catarrhini;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Email: cgapBe-remail.nih.gov
Tissue Procurement: ATCC/DCTD/DTP
CDNA Library Preparation: Ling Hong/Rubin Laboratory
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: LLCM1720 row: d column: 16
High quality sequence stop: 748.
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National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished (1999)
   /clone_lib="RIKEN full-length enriched, adult male nypothalamus"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  26.2%; Score 37.4; DB 2; Length 644; 64.4%; Pred. No. 17;
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0; Mismatches
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/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="IMAGE:4861407"
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Homo sapiens
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1 (bases 1 to 920)
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heb 56; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match
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ORGANISM
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Matches
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TITLE
JOURNAL
COMMENT
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BG764368
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Uniter: Duministon

Submitted (102-JUN-1999) Genoscope - Centre National de Sequencage:
BP 191 91006 EVRY cedex - FRANCE (E-mail : seqrefégenoscope.cns.fr
- Web: www.genoscope.cns.fr)

Determination of this BAC-end sequence was carried out as part of a collaboration with the Berkeley Drosophila Genome Project (BDGP).

The BDGP is constructing a physical map of the Drosophila melanogaster genome using these BACs. For further information please see http://www.fruifily.org The BDGP Drosophila melanogaster BAC library was prepared by Kazutoyo Gosegawa and Aaron Mammoser in Pieter de Jong's laboratory in the Department of Cancer Genetics at the Roswall Park Cancer Institute in Buffalo, NY. The library is named RPCI-98 and was constructed by partial EcoRI digestion of Drosophila DNA provided by the BDGP From the isogenic strain y2, cn bw sp, the same strain used for the BDGP's Pl and EST libraries. A more detailed description of the library and how to order individual BAC clones, the entire library, or filters for hybridization from the BACPAC Resource Center can be found at http://bacpac.med.buffalo.edu/drosophila_bac.htm.
CNS0072Q 932 bp DNA linear GSS 03-JUN-1999
Drosophila melanogaster genome survey sequence T7 end of BAC #
BACR14B09 of RPCI-98 library from Drosophila melanogaster (fruit
                                                                                                                                                                                                                                                                                                                                                                                              Eukaryota; Metazoa, Arthropoda; Hexapoda; Insecta; Pterygota;
Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
Ephydroidea; Drosophilidae; Drosophila.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            DB 10; Length 932;
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Pred. No. 34;
                                                                                                                                                                                                                                                                                                                 Drosophila melanogaster (fruit fly)
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/db_xref="taxon:7227"
/clone="BACR14B09"
/clone_lib="RRPCI-98"
/note="end : T7"
                                                                                                                             fly), genomic survey sequence.
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Anote="Vector: pBluescript II SK-; Site_1: EcoRI; Site_2: XhoI; This library, constructed by John Davies and Jeffrey McDermott, combines colbas from CC-1690 cells grown to mid-log phase in TAP (acetate-containing) medium in the light, TAP medium in the dark, HS (minimal) medium in the light, TAP medium in the dark, HS (minimal) medium in ambient levels of CO2 and HS medium bubbled with 5% CO2. PolyA mRNA was purified from each sample, pooled and CDNA synthesized. The CDNA was directionally cloned into lambda ZAP II (Stratagene) in the EcoRI (5') and XhoI (3') sites. pBluescript II SK- plasmids were exclsed from the lambda ZAP clones by superinfection with ExAssist (Stratagene) phage. The library was normalized using method 4 described in Bonaldo et al (1996) Genome Research 6: 791-806."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SAIL 781 E02.v2 SAIL Collection Arabidopsis thaliana genomic clone SAIL 781 E02.v2, genomic survey sequence. CL507458 CL507458.1 GI:46004778
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /organism="Chlamydomonas reinhardtii"
mol_type="mRNA"
fstrain="CC1690 wild type mt+ 21gr"
/strain="cC1690 wild type mt+ 21gr"
/db xref="taxon:3055"
/clone_lib="C. reinhardtii CC-1690, normalized, Lambda Zap
                            BI531460
1024113H09.yl C. reinhardtii CC-1690, normalized, Lambda Zap II
Chlamydomonas reinhardtii cDNA, mRNA sequence.
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Arabidopsis thaliana
Eukaryota, Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Agnoliophyta; eudicotyledons; core eudicotyledons;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   8 CTCCCTCTCTGCGCGCTCGCTCGCTCGGTGGGGCCTGCGGACCAAAGGTCCGCAGACGGC 67
                                                                                                                                                                                                                                                                          Gaps
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Pred. No. 43;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Vascular Plants. Project: 1024b
Unpublished (2001)
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Chlamydomonas reinhardtii
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Contact: Charles Hauser
DCMB Box 91000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Tel: 919 613 8159
Fax: 919 613 8177
Email: chauser@duke.edu
                                                                                                                                                         BI531460.1 GI:15372034
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Durham, NC 27708-1000
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/ Mol_type="mRNN"
/ Mb xref="taxon:9606"
/ Clone="IMAGE:6258293"
/ Clone="IMAGE:625829"
/ Lissue type="melanotic melanoma, cell line"
/ Lissue type="melanotic melanoma"
/ Lissue type="melanotic melanoma"
/ Lissue type="melanotic melanoma"
/ Note="Organ: skin, Vector: pOTB7; Site 1: XhoI; Site 2:
/ Note="Organ: skin, Vector: pOTB7; Site 1: XhoI; Site 2:
/ Note="Organ: skin, Vector: pOTB7; Site 1: XhoI; Site 2:
/ Note="Organ: skin, Vector: poTB7; Site 1: XhoI; Site 2:
/ Note="Organ: skin, Vector: poTB7; Site 1: XhoI; Site 2:
/ Note="Melanotic Closed complete colored colore
                                                                                                                                                                                                                                                                                                                                                                       BUBJ8990 1021 bp mRNA linear EST 16-OCT-2002 AGENCOURT 8209888 NIH_MGC_112 Homo sapiens cDNA clone IMAGE:6258289 5', mRNA Fequence.
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Email: cgapbs-r@mail.nlh.gov
Tissue Procurement: DCTD/DTP
CDNA Library Preparation: Rubin Laboratory
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LINL)
DNA Sequencing by: Agencourt Bioscience Corporation
Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LINL at:
http://image.llnl.gov
Place: Lich2413 row: p column: 02
High quality sequence stor: 36
High quality sequence stor: 231.
                                                                                                   4 CCCACTCCCTCTCTGCGCGCGCTCGCTCGGTGGGGCCTGCGGACCAAAGGTCCGCAGA 63
                                                                63
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1 (bases 1 to 1021)

1 (bases 1 to 1021)

Nath-MOC http://mgc.nci.nih.gov/.

National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished (1999)
                                                         4 CCCACTCCCTCTCTGCGCGCTCGCTCGCTCGGTGGGGCCTGCGGACCAAAGGTCCGCAGA
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   40; Indels
   32; Mismatches
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Homo sapiens
   41; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Syngenta Biotechnology Inc.
3054 Cormalis Rd., Research Triangle Park, NC 27709, USA
Email: allen.sessions@syngenta.com
BRC Stock Number C88349767; T-DNA left border flanking sequences of
Syngenta Arabidopsis Insertion Library (SAIL) lines are available
through the Arabidopsis Biological Resource Center (ABRC).
Sequences represent a pool of amplified genomic regions and not
single contiguous sequences.
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Contact: Yoshihide Hayashizaki
Laboratory for Genome Exploration Research Group, RIKEN Genomic
Sciences Center(GSC), Yokohama Institute
The Institute of Physical and Chemical Research (RIKEN)
1-7-22 Suehiro-cho, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Arakawa, T., Carninci, P., Fukuda, S., Furuno, M., Hanagaki, T., Arakawa, T., Carninci, P., Fukuda, S., Furuno, M., Kawai, T., Kamai, M., Kawai, T., Konno, H., Kouda, M., Koya, S., Matsuyama, T., Miyazaki, A., Nomura, K., Ohno, M., Okazaki, Y., Okido, T., Saito, R., Sakai, C., Sakai, K., Sano, H., Sasaki, D., Shibata, K., Shinagawa, A., Shiraki, T., Sogabe, Y., Suzuki, H., Tagamai, M., Tagawa, A., Takahashi, F., Tanaka, T., Toya, T., Muramatsu, M. and Hayashizaki, Y. RIKEN Mouse ESTS (Arakawa, T., et al. 2001)
                  (bases 1 to 1074)
Sessions, A., Burke, E., Presting, G., Aux, G., McElver, J., Patton, D.,
Sessions, A., Burke, E., Presting, G., Aux, G., McElver, J., Patton, D.,
Bullis, D., Shell, J., Miguel, T., Hutchison, D., Kimmerly, B.,
Mitzel, T., Katagiri, R., Glazebrock, J., Law, M. and Goff, S.A.
A high-throughput Arabidopsis reverse genetics system
Plant Cell 14 (12), 2985-2994 (2002)
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Mammalia, Eutheria, Euarchontoglires, Glires, Rodentia,
Sclurognathi, Muroidea, Muridae, Murinae, Mus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /clone="SAIL_781_E02.v2"
/clone lib="SAIL_Collection"
/note="T-DNA left border sequences were isolated using
modified TAIL-PCR strategy"
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1 Similarity 57.7%; Pred. No. 43;
64; Conservative 0; Mismatches 47;
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/ecotype="Columbia"
/db_xref="taxon:3702"
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Applied Trait Genetics
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Fax: 81-9-9212.

Email: genome-resegec.riken.jp, URL:http://genome.gec.riken.jp/
Carninci, P., Shibata, Y., Hayatsu, N., Sugahara, Y., Shibata, K.,
Itoh, M., Konno, H., Okazaki, Y., Muramatau, M. and Hayashizaki, Y.
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Watshiki, M., Yoneda, Y., Ishikawa, T., Ozawa, K., Tanak, T.,
Matsuuras, S., Kawai, J., Okazaki, Y., Muramatsu, M., Inoue, Y., Kira, A.
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Hayashizaki, Y.
Computational hanalysis of Full-Length Mouse cDNAs Compared with
Human Genome Sequences. Mamm. Genome. 12, 673-677 (2001)
Please visit our web site (http://genome.gsc.riken.go.jp) for
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cerebellum"
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/organism="Mus musculus"
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Submitted (02-A0G-2001) Asao Fujiyama, The Institute of Physical and Chemical Research (RIKEN), Genomic Sciences Center (GSC); 1-7-22 Suehiro-chou, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan (E-mail:chimpbes@gasc.riken.go.jp, URL:http://hgp.gsc.riken.go.jp/, Tel:81-45-503-9111, Fax:81-45-503-9170)
Clones are derived from the chimpanzee BAC library PTB This BAC end was generated during the R&D process and may have higher chance of clone tracking errors.
                                                                Pujyama, A., Hattori, M., Toyoda, A., Taylor, T.D., Yada, T.,
Totoki, Y., Watanabe, H. and Sakaki, Y.
Totoki, Y., Watanabe, H. and Sakaki, Y.
Direct Submission
Submitted (O2-MUG-2001) Asao Fujiyama, The Institute of Physical
and Chemical Research (RIKEN), Genomic Sciences Center (GSC);
1-7-22 Suehiro-chou, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan
(E-mall:chimpes@gsc.riken.go.jp, URL:http://hgp.gsc.riken.go.jp/,
Tel:81-45-503-9111, Fax:81-45-503-9170)
Clones are derived from the chimpanzee BAC library PTB This BAC end
was generated during the R&D process and may have higher chance of
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Pan troglodytes DNA, clone: PTB-066PlO.F, genomic survey sequence.
AG074763
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Ban troglodytes
Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Euarchontoglires, Primates, Catarrhini,
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Fuljvam, A., Hattori, M., Toyoda, A., Taylor, T.D., Yada, T.,
Totoki, Y., Matanabe, H. and Sakaki, Y.
Direct Submission
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BAC end sequences of Library PTB
Unpublished
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/organism="Pan troglodytes"
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/db_xref="taxon:9598"
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  sequences of Library PTB
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                           Unpublished
2 (bases 1 to 1123)
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R.Site 1
R.Site 2
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Matches 60; Conserv
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BF578052 860 bp mRNA linear EST 12-DEC-2000 600094705F1 NCI_CGAP_CO24 Mus musculus cDNA clone IMAGE:4209097 5',
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Pan troglodytes DNA, clone: PTB-076K10.R, genomic survey sequence.
AG080476
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S NIH-MGC http://mgc.nci.nih.gov/.
National Tinstitutes of Health, Mammalian Gene Collection (MGC)
L Unpublished (1999)
Contact: Robert Strausberg, Ph.D.
Email: cgapbs-rémail.nih.gov
Tissue Procurement: Jeffrey E. Green, M.D.
CDNA Library Preparation: Life Technologies, Inc.
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: LLAM9774 row: i column: 02
High quality sequence stop: 599.
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/clone="IMAGE:420909"

/lab_hole="DH10B (T1 phage-resistant)"

/clone lib="NCI CGAP Co24"

/note="Organ: colon; Vector: pCMV-SPORT6; Site_1: Not1;

Site_2: Sall; Cloned unidirectionally. Primer: Oligo dT.

Average insert size 1.6 kb. Constructed by Life

Technologies. Note: this is a NCI_CGAP Library."
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Pan troglodytes
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
                                                                                                                                                                                         Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia;
Sciurognathi; Muroidea; Muridae; Murinae; Mus.
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Totoki,Y., Watanabe,H. and Sakaki,Y.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1. .860
/organism="Mus musculus"
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                                                                                                                                             Mus musculus (house mouse)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  AG080476.1 GI:16632278
                                                                                              BF578052.1 GI:11651764
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                                                   mRNA sequence.
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Best Local Similarity
Matches 69; Conserva'
                                                                                                                                                                     Mus musculus
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Direct Submission.

Submitted (02-JUM-1999) Genoscope - Centre National de Sequencage:
BP 191 91006 EVRY cedex - FRANCE (E-mail : segref@genoscope.cns.fr
- Web: www.genoscope.cns.fr)
- webetwination of this BAC-end sequence was carried out as part of a collaboration with the Berkeley Drosophila Genome Project (BDGP).

The BDGP is constructing a physical map of the Drosophila melanogaster genome using these BACs. For further information please see http://www.fruitfly.org The BDGP Drosophila melanogaster BAC library was prepared by Kazutcyo Geoegawa and Aaron Mammoser in Pieter de Jong's laboratory in the Department of Cancer Genetics at the Roswell Park Cancer Institute in Biffalo, NY. The library is named RPCI-98 and was constructed by partial Ecord digestion of Drosophila DNA provided by the BDGP from the isogenic strain y2; cn bw sp, the same strain used for the BDGP's pl and BST libraries. A more detailed description of the library and how to order individual BAC clones, the entire library, or filters for hybridization from the BACPAC Resource Center can be found at http://bacpac.med.buffalo.edu/dxosophila_bac.htm.
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Drosophila melanogaster genome survey sequence TET3 end of BAC #
BACR11P16 of RPCI-98 library from Drosophila melanogaster (fruit
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Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
Ephydroidea; Drosophilidae; Drosophila.
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            Score 35; DB 10; Length 724;
Pred. No. 70;
                                                                               55; Indels
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/mol_type="genomic DNA"
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/clone="BACR11P16"
/clone lib="RRC1-98"
/note="end : TET3"
                                                                               0; Mismatches
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I (bases I to 74)

Kim, H. Yu, Y. Stum, D., Yost, D., Rao, K., Luo, M., Jetty, R., Kudrna, D., Muller, C., Hatfield, J., Soderlund, C. and Wing, R.
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                                                                                                                                                                                                                                                                   /mol_type="genomic DNA"
/db_xref="taxon:9598"
/clone="PTB-066810.F"
/sex="male"
/cell type="lymphoblast"
/cell type="lymphoblast"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Unpublished (2004)
Contact: Rod A. Wing
Arizona Genomics Institute
University of Arizona
Ferbes Building Room 303, Tucson, AZ 85721-0036, USA
Tel: 520 621 1259
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BACKWARD: CAC TCA TTA GGC ACC CCA
Insert Length: 161 Std Error: 0.00
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Seg primer: TAA TAC GAC TCA TAG GG
Class: BAC ends.
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Location/Qualifiers
1. .2024
/organism="Pan troglodytes"
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msh2_1301.x1 msh Pseudomonas aeruginosa genomic clone msh2_1301,
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B2570288.1 GI:27205349
GSS.
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Pseudomonas aeruginosa

Bacteria; Portecbacteria; Gammaproteobacteria; Pseudomonadales;
Bacteria; Portecbacteria; Gammaproteobacteria; Pseudomonadaceae; Pseudomonas

E 1 (bases 1 to 1303)

S pencer, D. H., Raymond, C.K., Smith, E.E., Sims, E.E., Hastings, M., Spencer, D. H., Raymond, C.K., Smith, E.E., Sims, E.E., Hastings, M., Whole-Genome-Sequence variation among multiple isolates of Psedomonas aeruginosa library

L Whole-Genome-Sequence variation among multiple isolates of Psedomonas aeruginosa library

L Sacterio. (2002) In press
Contact: Chris K. Raymond
Genome Center
University of Washington
Box 352145, Seattle, WA 98105-2145, USA
Tel: 2062857244
Fax: 2066857244
Email: craymond@u.washington.edu
Class: shotgun.
Location/Qualifiers
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550 BSSSSVGMGCACSSASSVSCBBSSVASSVSSGBVSRGCGRCVGGGVGGGSRVSSCSSGSS 609
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/mol_type="genomic DNA"
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/db_xref="taxon:287"
/clone="msh2_1301"
/clone="msh2_1301"
/note="lib="msh"
/note="Environmental isolate. Whole genomic shotgun library."
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Adg39763 AAV-6 gen
Ad276509 Adeno-a88
Ad113985 Adeno-a88
Adg39759 AAV-3A gen
Adg39760 Adeno-a88
Adg39764 AAV-7 gen
Adv67509 Nuclectid
Adv67509 Nuclectid
Adv67509 Nuclectid
Adv67509 Adeno-a88
Adv93254 Inverted
Adv6769 Double-D
Aat4962 Adeno a88
Adv77279 Nuclectid
Adv77279 Nuclectid
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Add3535 Inverted
Adv77279 Nuclectid
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Abs6989 Human ade
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/*tag= a
/labal= 5'_TTR
/note= "Inverted terminal repeat which is capable of
forming T-shaped hairpin structure"
89. .110
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/note= "Terminal resolute site (TRS)"
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124. .125
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370. .275
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          ADG39763
ADE76509
ADG39759
ADG39764
ADZ27030
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ACF35677
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ADM32254
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AATG3404
AATG3604
AAT
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/bound_moiety= "USF"
/note="E box"
236. .299
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/label= P5_TATA-Box
299. .306
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               misc_feature
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Ad113984 Adeno-ass
Ad39758 AAV-1 gen
Ad939764 AAV-7 gen
Adv67509 Nucleotid
Ad227010 Adeno-ass
Ad23749 AAV6 DNA
Ad113981 Adeno-ass
Ad23749 AAV6 DNA
Ad13981 Adeno-ass
Ad60781 Adeno-ass
Ad60772 Adeno-ass
Ad60772 Adeno-ass
Ad13984 Adeno-ass
Ad13984 Adeno-ass
Ad1399758 AAV-1 gen
Ad1399758 AAV-1 gen
Ad13984 Adeno-ass
Ad1399758 AAV-1 gen
Ad1399758 AAV-1 gen
Ad1399758 AAV-1 gen
Ad23759 AAV-1 gen
Ad23758 AAV-1 gen
Ad1399758 AAV-1 gen
                                                                                                                                                                                       November 28, 2005, 08:46:14; Search time 66.9124 Seconds (without alignments) 14243.261 Million cell updates/sec
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                                                                                                                                                                                                                                                                                                                  143
1 ttacccctagtgatggagtt......cgcagagagggagtgggcaa 143
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       9993994
                                       GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    of hits satisfying chosen parameters:
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Maximum Match 100%
Listing first 45 summaries
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ADC39758
ADC39758
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ADZ27030
AAD00781
AAF23749
ADC39763
AAD00772
ADD00781
AAD00772
ADD13984
AAF23749
ADC13984
                                                                                                                                          - nucleic search, using sw model
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Gapop 10.0 , Gapext 1.0
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The present sequence is an adeno-associated virus serotype 1 (AAV-1) DNA characterised by two inverted terminal repeats (ITR) and open reading frames for rep and capsid (cap) proteins. The rep reading frame encodes four proteins, Rep 78, Rep 68, Rep 52 and Rep 40, while the cap reading frame encodes three structural proteins, VP1, VP2 and VP3. The AAV-1 sequence or its fragments particularly ITRs, rep and cap coding regions, are useful in production of recombinant viral vectors for gene delivery. These vectors can be used as gene therapy vectors, vaccine vectors or antisense delivery vectors. The AAV-1 does not induce the formation of neutralising antibodies specific to any serotype of AAV hence is useful for transforming host cells, and in the preparation of a medicament for the delivery of transgene to a host
                                                                                                                                                                                                                                                                                                                                                                                                                                                               9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           adeno-associated virus; AAV; cytostatic; antipsoriatic; antirheumatic;
WPI; 2000-376571/32.
P-PSDB; AAY71161, AAY71164, AAY71165, AAY71166, AAY71167, AAY71168,
                                                              Novel adeno-associated virus serotype 1 polynucleotide useful for preparation of medicament for delivery of a transgene to a host.
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                                                                                                                                                                                                                                                                                                                                                              Sequence 4718 BP; 1121 A; 1393 C; 1273 G; 931 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                               Length 4718;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           autoimmune thyroiditis; scleroderma; Crohn's disease; gene;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         antiarthritic, neuroprotective, antidiabetic, antithyroid, decameloogical, antiinflammatory, gene therspy, vaccine, hyperproliferative, cancer, pacriasis, autoimmune disease; rheumatoid arthritis, multiple sclerosis, diabetes;
                                                                                                                                                                                                                                                                                                                                                                                                                               Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Adeno-associated virus (AAV) related DNA, SEQ ID No 6.
                                                                                                                                                                                                                                                                                                                                                                                           100.0%; Score 143; DB 3;
100.0%; Pred. No. 3.6e-28;
11ve 0; Mismatches 0;
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                                                                                                                   Claim 1; Fig 1; 108pp; English
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17-DEC-2001; 2001US-0341117P.
01-MAY-2002; 2002US-0377066P.
05-JUN-2002; 2002US-038675P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        12-NOV-2002; 2002EP-00257826
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                                                                                                                                                                                                                                                                                                                                                                                                            Local Similarity 100.
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                                                                                                                                                                                                                                                                                                                                                                                                Query Match
                                   AAY71169
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Matches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              note "This region interrupts the coding sequence of Rep is and Rep 40"
                                                                                                                                                                                                                                                                                                                              /product "Rep 40"
/function "regulates replication and integration of AAV
/function bus tell's chromosome"
/note "The coding region is interrupted by intron"
                                                                                 /function= "regulates replication and integration of AAV DNA into host cell's chromosome"
                                                                                                                                                        /product= "Rep 78"
/function= "regulates replication and integration of AAV
DNA into host cell's chromosome"
                                                                                                                                                                                                                                                                                                                                                                                                                                                             /function= "regulates replication and integration of AAV DNA into host cell's chromosome"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /label= 3'_ITR
/note= "Inverted terminal repeat which is capable of
forming T-shaped hairpin structure"
                                                                                                                 note= "The coding region is interrupted by intron" 
135. .2206
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            protein"
protein"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /product= "VP1 protein"
/note= "Capsid protein"
2634. .4433
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            protein"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /*tag= p
/label= P40_TATA-BOX
1875. .1876
/*tag= h
/note= "YY1/p5 RNA"
335. .2272
                                                                                                                                                                                                                              *tag= 1
|abel= P19_TATA_Box
                                                                                                                                                                                                                                                                                                                                                                                                                                              products "Rep 52"
                                                                product= "Rep 68"
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/*tag= m
/note= "P19 RNA"
1007. .2272
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924. .2220
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/product= "VP3 p
/note= "Capsid p
4447. .4452
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note= "Capsid
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4576. .
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Philpott N;

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WPI; 2003-833723/77
          Falck-Pedersen ES,
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ADG39758
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                                                                                                                     The invention relates to a novel method for detecting adeno-associated virus (AAV) sequences in a sample, which comprises subjecting a sample containing a DNA to amplification via a polymerase chair reaction (PCR). The AAV sequence have the following activities: cytostatic, antitheumatic, antiarthritic, neuroprotective, antidiabetic, antithyroid, dermatological, and antiinflammatory. The AAV sequence can be used in gene therapy or as part of a vaccine to treat disorders. The method is useful in detecting and/or identifying AAV sequences may be used e.g. for preventing or treating hyperproliferative conditions such as cancers and psoriasis, and other autoimmune diseases like rheumatoid arthritis, multiple sclerosis, diabetes, autoimmune diseases thy proporties.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ss; cytostatic; neuroprotective; antiinflammatory; gene therapy; expression construct; adeno-associated virus; thregration efficiency element; inverted terminal repeat; integration; chromosome; cancer; lymphoma; leukemia; multiple myeloma; neuroblastoma; retinoblastoma; inflammatory disease; arthritis;
                                         Detecting adeno-associated virus sequences in a sample, useful for e.g. preventing or treating hyperproliferative or autoimmune diseases, comprises subjecting a sample having a DNA to amplification via polymerase chain reaction.
                                                                                                                                                                                                                                                                                                                                                                                   Gaps
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                                                                                                                                                                                                                                                                                                  Sequence 4718 BP; 1121 A; 1393 C; 1273 G; 931 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                          Length 4718;
                                                                                                                                                                                                                                                                                                                                               Indels
                                                                                                                                                                                                                                                                          represents an AAV related DNA sequence of the invention.
                                                                                                                                                                                                                                                                                                                       Query Match 100.0%; Score 143; DB 10;
Best Local Similarity 100.0%; Pred. No. 3.6e-28;
Matches 143; Conservative 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Adeno-associated virus serotype 1 complete DNA
                                                                                                     Claim 14; SEQ ID NO 6; 419pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              4696 GCGCGCAGAGAGGGAGTGGGCAA 4718
                                                                                                                                                                                                                                                                                                                                                                                                                                                               GCGCGCAGAGAGGGAGTGGGCAA 143
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  Alvira M;
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  Wilson JM,
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  Gao G,
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caid sequence encoding an adeno-associated virus integration efficiency clement (AAV IEE), which is devoid of AAV inverted terminal respeats (AAV INVerted serminal respeats (AAV INVerted serminal respects (AAV INVerted serminal respects (AAV INVerted serminal respects (AAV INVerted serminal respects (AAV INVERD STORE) and site-specially integrates into a head cell chromosome when provided to the host cell in conjunction with an AAV Rep protein. The carcer, renal cancer, and cancer, including lung cancer, colon cancer, renal cancer, spinal chord cancer, bladder cancer, brain cancer, spinal chord cancer, breast cancer, cervical cancer, lymphoma, endometrial cancer, laryngeal cancer, pastrointeetinal cancer, laryngeal cancer, prostatic cancer, multiple myeloma, neuroblastoma, ovarian cancer, pastrointeetinal cancer, stomach cancer, thymus cancer tryoid cancer. Other pathologic state includes inflammatory disease (arthritis), neurodegenerative disease a disease of an organ attributed to the presence of increased or decreased level of a particular gene product(s). This sequence
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New expression construct comprising a nucleic acid sequence encoding an adeno-associated virus integration efficiency element, useful for treating cancer e.g. lung cancer or colon cancer or inflammatory disease
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   parvovirus; rep; cap; DNA binding domain; capsid interacting domain; recombinant hybrid parvovirus particle; recombinant adeno-associated virus; rAAV; AAV; vaccine; gene therapy;
                                                                                                                                                                                                                                                                    invention relates to an expression construct comprising a nucleic
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   100.0%; Score 143; DB 10; Length 4718; 100.0%; Pred. No. 3.6e-28; ive 0; Mismatches 0; Indels 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 4718 BP; 1121 A; 1393 C; 1273 G; 931 T; 0 U; 0 Other;
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                                                                                                                                                                                           Disclosure; SEQ ID NO 3; 62pp; English
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Matches 143; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Adeno-associated virus
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ID ADG3
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AC ADG3
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DT 11-N
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                                                                                                                                                                                                                             The present invention describes a polynucleotide (I), comprising parvovirus rep coding sequences and parvovirus cap coding sequences and parvovirus cap coding sequences encodes a DNA binding domain from a first parvovirus. The cap coding sequence comprises sequences from the first parvovirus. The cap coding sequence comprising (I); or parvovirus and a vector comprising (I); or parvovirus rep coding sequences and parvovirus from a parvovirus and a capsid interacting commain from a first parvovirus and a capsid interacting commain from a first parvovirus and a capsid interacting coding sequences comprises sequences from the different parvovirus, and the rep coding sequences are stably integrated into the genome of the coding sequences are stably integrated into the genome of the cap coding sequences are stably integrated into the genome of the cap coding sequences are stably integrated into the genome of the cap coding sequences are stably integrated into the genome of the cap coding sequences are stably integrated into the genome of the cap coding sequences are stably integrated into the genome of the capsociated virus (rAAV) particle. (I) can be used in producing higher stocks of hybrid parvoviruses or parvovirus vectors, which may be used in producing physecond the symptoms associated with any disorder related to gene expression. The polynucleotide may be used to produce a parvovirus vector companies and in vitro or in vivo, or in diagnostic and sereening methods. The present sequence is used in the exemplification of the
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antiarthritic; neuroprotective; antidiabetic; antithyroid;
dermatological; antiinflammatory; gene therapy; vaccine;
                                                                                                                                New polynucleotides comprising parvovirus rep coding sequences and parvovirus cap coding sequences, useful in producing higher stocks of hybrid parvovirus vectors for delivering therapeutic nucleic acids to
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Length 4718;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match
100.0%; Score 143; DB 12;
Best Local Similarity 100.0%; Pred. No. 3.6e-28;
Matches 143; Conservative 0; Mismatches 0;
                                                                                                                                                                                                        Disclosure; SEQ ID NO 20; 115pp; English.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ADE76502 standard; DNA; 4721 BP
             18-DEC-2001, 2001US-0341919P.
                                         (UYNC-) UNIV NORTH CAROLINA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             29-JAN-2004 (first entry)
                                                                                                   WPI; 2004-062324/06.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             present invention.
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The invention relates to a novel method for detecting adeno-associated virus (AAV) sequences in a sample, which comprises subjecting a sample containing a DNA to amplification via a polymerase chain reaction (PCR). The AAV sequence have the following activities: cytostatic, antithermatic, antithermatic, antiarthritic, neuroprotective, antidiabetic, antithermatic, antiarthritic, neuroprotective, antidiaperson of a manufalabetic, antichermatic, antiarthritic, neuroprotective, antidiaperson of a match of a part of a vaccine to treat equence an be used in gene lherapy or as part of a vaccine to treat equences and isolating novel sequences that are identified. The sequences may be used e.g. for preventing or treating hyperproliferative conditions such as cancers and psoriasis, and other autoimmune diseases like rheumatoid arthritis, multiple sclerosis, diabetes, autoimmune thyroiditis, scleroderma or Crohn's disease. This polynucleotide sequence represents an AAV related DNA sequence of the invention.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Detecting adeno-associated virus sequences in a sample, useful for preventing or treating hyperproliferative or autoimmune diseases, comprises subjecting a sample having a DNA to amplification via polymerase chain reaction.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           'Match 94.8%; Score 135.6; DB 10; Length 4721; Local Similarity 97.2%; Pred. No. 3.1e-26; les 138; Conservative 0; Mismatches 4; Indels 0;
                                                                                    ds.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 4721 BP; 1108 A; 1405 C; 1301 G; 907 T; 0 U; 0 Other;
hyperproliferative, cancer; psoriasis; autoimmune disease; rheumatoid arthritis; multiple sclerosis; diabetes; autoimmune thyroiditis; scleroderma; Crohn's disease; gene;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Claim 17; SEQ ID NO 1; 419pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            4700 CGCGCATAGAGGGAGTGGCCAA 4721
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Alvira M;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             13-NOV-2001; 2001US-0350607P.
17-DEC-2001; 2001US-0341117P.
01-MAX-2002; 2002US-0377066P.
05-JUN-2002; 2002US-038675P.
                                                                                                                                                                                                                                                                                                                                                                                                                 12-NOV-2002; 2002EP-00257826
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    11-MAR-2004 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   (UYPE-) UNIV PENNSYLVANIA.
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                                                                                                                                                                    Adeno-associated virus 7.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    WPI; 2003-450984/43.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    G, Wilson JM,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          P-PSDB; ADE76503
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antiarteriosclerotic; antilipemic; gene therapy; cholesterol; apolipoprotein B; apoE; apolipoprotein A; apoA; atherosclerosis; lipoprotein defect; ss.

825. .3049 /*tag= b /note= "encodes vp1"

234. .3049

misc_feature

misc_feature

*tag=

Location/Qualifiers

Adeno-associated virus.

....107 /*tag= a /note= "5' ITR"

repeat_region

Key

misc_feature

.434. .3049 /*tag= d /note= "encodes vp3" note= "encodes vp2"

/*tag= e /note= "3' ITR"

WO2004108922-A2

16-DEC-2004.

.4721

4704.

repeat_region

23-APR-2004; 2004WO-US010965 25-APR-2003; 2003US-0465293P

UYPE-) UNIV PENNSYLVANIA.

Nucleotide sequence of AAV serotype 7.

(first entry)

10-MAR-2005

ADV67509;

ADV67509 standard; DNA; 4721 BP.

RESULT 7 ADV67509

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The present invention describes a polynucleotide (I), comprising parvovirus rep coding sequences and parvovirus cap coding sequences. The parvovirus and a capsid interacting domain from a first ferent caps encodes a DNA binding domain from a first ferent parvovirus. The cap coding sequence comprises sequences from the different parvovirus. Also described: (I) a vector comprising (I); (2) a cell comprising (I), or parvovirus rep coding sequences and parvovirus cap coding sequences. ONA binding domain from a first parvovirus rep coding sequences are comprised in the cap coding sequences comprised in the cap coding sequences are stably integrated into the genome of the coding sequences are stably integrated into the genome of the cell; and (3) producing a recombinant hybrid parvovirus particle or adenocasociated virus (rAAV) particle. (I) can be used in producing higher seconds of hybrid parvoviruses or parvovirus vectors, which may be used in the delivery of nucleic acids having bological effect to treat or ameliorate the symptoms associated with any disorder related to gene expression. The polynucleotide may be used to produce a parvovirus vector comprises an immunogenic polypeptide in a subject, e.g. for vaccination. The parvovirus vector may also be used to produce a parvovirus vector acid to a cell in vitro or in vivo, or in diagnostic and screening methods.
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                                                                          parvovirus; rep; cap; DNA binding domain; capsid interacting domain; recombinant hybrid parvovirus particle; recombinant adeno-associated virus; rAAV; AAV; vaccine; gene therapy;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  New polynucleotides comprising parvovirus rep coding sequences and parvovirus cap coding sequences, useful in producing higher stocks hybrid parvovirus vectors for delivering therapeutic nucleic acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 4721 BP; 1108 A; 1405 C; 1301 G; 907 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Disclosure; SEQ ID NO 26; 115pp; English.
AAV-7 genomic DNA sequence SEQ ID NO:26
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  02-DEC-2002; 2002WO-US038423
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          18-DEC-2001; 2001US-0341919P
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              (UYNC-) UNIV NORTH CAROLINA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Samulski RJ, Rabinowitz JE;
                                                                                                                                                                                                                                                                                                              Adeno-associated virus 7.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          WPI; 2004-062324/06.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         present invention.
                                                                                                                                                                                                                                                                                                                                                                                                      WO2003104392-A2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              18-DEC-2003
                                                                                                                                                                                                                                   gene; ds.
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The specification describes a method for lowering total cholesterol levels in a subject. The method comprises delivering to the subject a recombinant adeno-associated virus (AAV) comprising a gene encoding a human apolipoprotein E (apoE) or apoA under the control of a regulatory control sequence which directs expression of the gene. The recombinant AAV also comprises a capsid protein selected from an AAV serotype (e.g. AAV or AAV8) which preferentially expresses high levels of transgene in live. A therapeutically effective amount of apoB or apoA expression is obtained upon delivery of low dose of AAV. The method of the invention is useful for lowering total cholesterol levels in a subject, e.g. for treating atherosclerosis, and for correcting defects in lipoprotein. The present sequence represents AAV serotype 7 (AAV77), which may be used to
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Lowering total cholesterol levels and treating atherosclerosis in a subject comprises delivering a recombinant adeno-associated virus (AAV) comprising an AAV serotype capsid protein or a gene encoding human apolipoprotein B (apos) or apoA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Score 135.6; DB 14; Length 4721;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 4721 BP; 1108 A; 1405 C; 1301 G; 907 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           produce recombinant AAV vectors of the invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Disclosure; SEQ ID NO 7; 69pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     94.8%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Wilson JM;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                WPI; 2005-031700/03.
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Best Local Similarity
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Gaps

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4; Indels

DB 12; Length 4721;

94.8%; Score 135.6; DB 1 97.2%; Pred. No. 3.1e-26; 0; Mismatches

Query Match Best Local Similarity 97.2 Matches 138; Conservative

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Pred. No. 3.1e-26;

CGCGCATAGAGGGAGTGGCCAA 4721 CGCGCAGAGGGAGTGGGCAA 143

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                                                                                                                                                                                                              61
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       rheumatoid arthritis; multiple sclerosis; sarcoidosis; diabetes; scleroderma; psoriasis; vasculitis; Crohn's disease; hemophilia; HIV; bacterial infection; cancer; ulcerative colitis; antirheumatic; antiarthritic; neuroprotective; antillammatory; antidiabetic; antiarthritic; vasctropic; gastrointestinal-gen.; hemostatic; anti-HIV; virucide; antibacterial; cytostatic; antiulcer; dermatological; ds.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  New adeno-associated virus (AAV) clade comprising at least three AAV members, useful for preventing and/or treating arthritis, multiple sclerosis, diabetes, scleroderma, psoriasis, hemophilia, HIV, bacterial
                                                                      Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match 94.8%; Score 135.6; DB 14; Length 4721; Best Local Similarity 97.2%; Pred. No. 3.1e-26; Matches 138; Conservative 0; Mismatches 4; Indels 0;
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   4; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Vandenberghe LH;
   0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Adeno-associated virus DNA SEQ ID NO 180.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Claim 12; SEQ ID NO 180; 569pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                   4700 CGCGCATAGAGGGAGTGGCCAA 4721
                                                                                                                                                                                                                                                                                                                                                       122 CGCGCAGAGAGGGAGTGGGCAA 143
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ADZ27030 standard; DNA; 4721 BP
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                30-SEP-2003; 2003US-0508226P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             30-SEP-2004; 2004WO-US028817
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   30-JUN-2005 (first entry)
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Matches 138; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Adeno-associated virus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             infection and cancer.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   WPI; 2005-285437/29.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     WO2005033321-A2.
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                                                           Adeno-associated virus serotype 1; AAV-1; rep protein; capsid protein; cap protein; recombinant viral vector; gene delivery; gene therapy; vaccine; transgene; inverted terminal repeat; ITR; ss.
                           Novel adeno-associated virus serotype 1 polynucleotide useful for preparation of medicament for delivery of a transgene to a host.
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/*tag= a
/*tag= binds to nucleotides 85. .125"
42. .62
                                                                                                                                                                                                                                                                                                                         Adeno-associated virus serotype 1 5' inverted terminal repeat.
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                                                                                                                                        4700 CGCGCATAGAGGGAGTGGCCAA 4721
                                                                                                                        CGCGCAGAGAGGGAGTGGGCAA 143
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                                                                                                                                                                                                                                AAD00781 standard; DNA; 143
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/*tag= c
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misc_binding
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                                                                                                                                                                         present sequence is the DNA sequence of one such serotype (AAV6). AAV6 can be used to contruct AAV viral vectors for use in gene therapy for a range of disorders: cystic fibrosis, cancer, AIDS, atherosclerosis, sickle cell anaemia, thalassaemia, blood clotting disorders and diabetes. The AAV viral vectors have increased transduction efficiency of a particular host cell as the AAV viron containing the AAV vector genome can be modified to express a capid protein of an AAV serotype that transduces the selected host cell
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       present invention relates to adeno-associated virus serotypes. The
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                                                                                                                   19 TTGCCCACTCCCTCTCTGCGCGCTCGCTCGGTGGGGCCTGCGGACCAAAGGTCCGC
                                                                                       Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Adeno-associated virus serotype 6 and viral vector derived from it gene therapy of cystic fibrosis, cancer, acquired immunodeficiency syndrome, sickle cell anemia, thalassemia and diabetes.
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                                                          Length 143;
                                                                                       Indels
   viral vector. The ITR forms a T-shaped hairpin structure
                                 Sequence 143 BP; 24 A; 50 C; 48 G; 21 T; 0 U; 0 Other;
                                                         Match
Local Similarity 100.0%; Pred. No. 1.6e-23;
es 125; Conservative 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                       AAF23749 standard; DNA; 4683 BP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Claim 1; Fig 1; 50pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    97US-00873168
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  97US-00873168
                                                                                                                                                                                                                                                                                                                                                                                                 28-MAR-2001 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Rutledge EA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            (UNIW ) UNIV WASHINGTON.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Adeno associated virus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       WPI; 2001-060164/07.
                                                                                                                                                                                                                                      GGCAA 143
                                                                                                                                                                                                                                                               121 GGCAA 125
                                                                                                                                                                                                                                                                                                                                                                                                                            AAV6 DNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      11-JUN-1997;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  11-JUN-1997;
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                                                            Query Match
Best Local S.
Matches 125
                                                                                                                                                                             96
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                                                                                                                                                                                                                                                                                                           RESULT 10
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85.2%; Score 121.8; DB 4; Length 4683; 98.4%; Pred. No. 1.3e-22; Artive 0; Mismatches 2; Indels 0;

Best Local Similarity 98.4 Matches 123; Conservative

Query Match

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The invention relates to an expression construct comprising a nucleic acid sequence encoding an adeno-associated virus integration efficiency clement (AAV IEEE), which is devoid of AAV inverted terminal repeats (AAV IEEE), which is devoid of AAV inverted terminal repeats (AAV IEEE) and site-specifically integrates into a host cell chromosome when provided to the host cell in conjunction with an AAV Rep protein. The concert can be used as a therapeutic factor for treating a mammal for a pathologic state which is cancer, including lung cancer, cohon cancer, renal cancer, spinal chord cancer, bladder cancer, lymphoma, endometrial cancer, beophageal cancer, cervical cancer, lymphoma, endometrial cancer, laryngeal cancer, leukemia, cancer, multiple myeloma, neuroblastoma, voraitan cancer, prostatic cancer, retinoblastoma, skin cancer, schoarch cancer, cancer, thymus cancer thyroid cancer. Other pathologic state includes inflammatory disease (arthritis), neurodegenerative disease, a disease of an organ attributed to the presence of increased or decreased level of a particular gene product(s). This sequence
                                                   ss; cytostatic; neuroprotective; antiinflammatory; gene therapy; expression construct; adeno-associated virus; integration efficiency element; inverted terminal repeat; integration; chromosome; cancer; lymphoma; leukemia; multiple myeloma; neuroblastcoma; retinoblastcoma; inflammatory disease; arthritis;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          New expression construct comprising a nucleic acid sequence encoding an adeno-associated virus integration efficiency element, useful for treating cancer e.g. lung cancer or colon cancer or inflammatory disease
                                                                                                                                                                                                                                                                                                                                                                                Adeno-associated virus serotype 6 complete DNA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Disclosure, SEQ ID NO 2; 62pp; English.
                                                                                                                                                                                                                                                                    ADL13983 standard; DNA; 4683 BP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Falck-Pedersen ES, Philpott N;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  (CORR ) CORNELL RES FOUND INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       09-APR-2003; 2003WO-US011191.
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                                                                                                                                                                                                                                                                                                                                           06-MAY-2004 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     neurodegenerative disease.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Adeno-associated virus 6.
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                                                                                                                                                                       4563 GGCAA 4559
                                                                                                                                  GGCAA 143
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              WO2003087334-A2
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   23-OCT-2003.
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WPI; 2000-376571/32.
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                                                                                                                                                                                                                                                                                                                                                                4563 GGCAA 4559
                                                                                                                                                                       Local Similarity
                                                                                                                                                                                                                                                                                                                                   GGCAA 143
                                                                                                   present invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     WO200028061-A2
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                                                                                                                                                            Query Match
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           The present invention describes a polymucleotide (1), comprising parvovirus rep coding sequences and parvovirus cap coding sequences. The rep coding sequences a DNA binding domain from a first parvovirus different from a first parvovirus. The cap coding sequences recording sequences a provirus, and a capsid interacting domain from a parvovirus different from the different parvovirus. Also described: (1) a vector comprising (1), cap coding sequences and parvovirus cap coding sequences in the parvovirus of first parvovirus and a capsid interacting command from a first parvovirus and a capsid interacting coding sequences comprise sequences from the different parvovirus, the cap coding sequences comprise sequences from the different parvovirus, and the rep coding sequences are stably integrated into the genome of the coling sequences are stably integrated into the genome of the coling sequences are stably integrated into the genome of the coling sequences are stably integrated into the genome of the coling sequences are stably integrated into the genome of the coling sequences are stably integrated into the genome of the coling sequences are stably integrated into the genome of the coling sequences are stably integrated into the genome of the coling sequences are stably integrated into the genome of the coling sequences (TAAV) particle. (1) can be used in vaccines, and in gene therapy. The polynucleotide (1) can be used in producing higher stocks of hybrid parvovirus particle. (2) can be used in producing higher seconds.
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                                                                                                 4683 TIGCCCACTCCTCTAIGCGCGCTCGCTCGGTCGGGGGCCTGCGGACCAAAGGTCCGC
                                                                                  19 TTGCCCACTCCCTCTCTGCGCGCTCGCTCGGTGGGGCCTGCGGACCAAAGGTCCGC
                                                       Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                  parvovirus; rep; cap; DNA binding domain; capsid interacting domain; recombinant hybrid parvovirus particle; recombinant adeno-associated virus; rAAV; AAV; vaccine; gene therapy;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         New polynuclectides comprising parvovirus rep coding sequences and parvovirus cap coding sequences, useful in producing higher stocks hybrid parvovirus vectors for delivering therapeutic nucleic acids subject.
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                           DB 10, Length 4683;
Sequence 4683 BP; 1114 A; 1363 C; 1277 G; 929 T; 0 U; 0 Other;
                                                       Indels
                           Score 121.0,
Pred, No. 1.3e-22;
                                                       0; Mismatches
                         85.2%; Score 121.8; 98.4%; Pred. No. 1.3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Disclosure; SEQ ID NO 25; 115pp; English.
                                                                                                                                                                                                                                                                                                                                                                                           AAV-6 genomic DNA sequence SEQ ID NO:25.
                                                                                                                                                                                                                                                                                                     ADG39763 standard; DNA; 4683 BP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              18-DEC-2001; 2001US-0341919P.
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                                                                                                                                                                                                                                                                                                                                                                (first entry)
                                       Best Local Similarity 98.4 Matches 123; Conservative
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                                                                                                                                                                                                                                4563 GGCAA 4559
                                                                                                                                                                                                     139 GGCAA 143
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                           Query Match
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  the delivery of nucleic acids having biological effect to treat or ameliorate the symptoms associated with any disorder related to gene expression. The polymuclectide may be used to produce a parvovirus vector to express an immunogenic polypeptide in a subject, e.g. for vaccination. The parvovirus vector and in vivo be used to provide an antisense nucleic acid to a cell in vitro or in vivo, or in diagnostic and screening methods. The present sequence is used in the exemplification of the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          138
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          protein; capsid protein;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                4683 Tracceaerecererardedederederederederedesederededadesandarecec
                                                                                                                                                                                                                                                                                                                                                                                                                               19 TIGCCCACTCCCTCTCTGCGCGCTCGCTCGGTGGGGCCTGCGGACCAAAGGTCCGC
                                                                                                                                                                                                                                                                                                                                                                           Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Adeno-associated virus serotype 1; AAV-1; rep protein; capsid prote cap protein; recombinant viral vector; gene delivery; gene therapy; vaccine; transgene; inverted terminal repeat; ITR; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Novel adeno-associated virus serotype 1 polynucleotide useful for preparation of medicament for delivery of a transgene to a host.
                                                                                                                                                                                                                                                                                                              DB 12; Length 4683;
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                                                                                                                                                                                                                                                            Sequence 4683 BP; 1114 A; 1363 C; 1277 G; 929 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Adeno-associated virus serotype 1 5' inverted terminal repeat.
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                                                                                                                                                                                                                                                                                                                                                                        Indels
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/bound_moiety= "binds to nucleotides 41.
                                                                                                                                                                                                                                                                                         Score 121.8; DB 12;
Pred. No. 1.3e-22;
Pred. No. 1.3e-22;
                                                                                                                                                                                                                                                                                                                                                                        0; Mismatches
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AAD00781 standard; DNA; 143 BP.
                                                                                                                                                                                                                                                                                                                85.2%;
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                                                                                                                                                                                                                                                                                                                                                                  Matches 123; Conservative
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/note = "This region interrupts the coding sequence of Rep is and Rep 40" (223. .4433
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /product= "Rep 52"
/function= "regulates replication and integration of AAV DNA into host cell's chromosome"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /function= "regulates replication and integration of AAV DNA into host cell's chromosome" /note= "The coding region is interrupted by intron" 1007. .2206
                                                                                                                                                                            /function= "regulates replication and integration of AAV DNA into host cell's chromosome" /note= "The coding region is interrupted by intron" 335. .2206
                                                                                                                                                                                                                                                                              /function= "regulates replication and integration of AAV DNA into host cell's chromosome"
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/label= 3' ITR
/label= 1 inverted terminal repeat which is capable of
forming T-shaped hairpin structure"
bound moiety= "YY1 factor" 770. .275
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  protein"
protein"
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protein"
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/note= "Capsid protein"
2634. .4433
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label=_P19_TATA_Box
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875. .1876
                                                                                          '*tag= h
'note= "YY1/p5 RNA"
135. .2272
                                     *tag= g
label= P5_TATA-Box
99. .306
                                                                                                                                                                                                                                                                         product= "Rep 78"
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1924. .2220
/*tag= k
                                                                                                                                                               product = "Rep 68"
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/*tag= m
/note= "P19 RNA"
1007. .2272
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/product= "VP3 p
/note= "Capsid p
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note= "Capsid
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                                                                       misc_feature
                                                                                                                                                                                                                                                                                                                                                                                     misc_feature
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                      TATA_signal
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                                                                                                                              CDS
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     The patent discloses an adeno-associated virus serotype 1 (AAV-1) DNA which is characterised by two inverted terminal repeats (TTR) and open reading frames for rep and capsid (cap) proteins. The rep reading frame encodes four proteins, Rep 78, Rep 68, Rep 52 and Rep 40, while the cap reading frame encodes three structural proteins, VPI, VP2 and VP3. The AAV-1 sequence or its fragments particularly ITRs, rep and cap coding regions, are useful in production of recombinant viral vectors for gene delivery. These vectors can be used as gene therapy vectors, vaccine vectors or antisense delivery vectors. The AAV-1 does not induce the formation of neutralising antibodies specific to any serotype of AAV hence is useful for transforming host cells, and in the preparation of a medicament for the delivery of transgene to a host. The present sequence is a 5. ITR of AAV-1 DNA which is useful in the production of recombinant viral vector. The ITR forms a T-shaped hairpin structure
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                1. .143
*tag= a
/label= 5'_ITR
/note= "Inverted terminal repeat which is capable of
forming T-shaped hairpin structure"
                                                                                                                                                                                                                                                                                                                                                                                          0; Gaps
                                                                                                                                                                                                                                                                                                                                                 Query Match
83.2%; Score 119; DB 3; Length 143;
Best Local Similarity 89.5%; Pred. No. 5.9e-22;
Matches 128; Conservative 0; Mismatches 15; Indels
                                                                                                                                                                                                                                                                                                                Sequence 143 BP; 24 A; 50 C; 48 G; 21 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   *tag= c
note= "Terminal resolute site (TRS)"
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bound moiety= "Rep protein"
24. .125
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/label= P5_promoter
237. .245
/*tag= f
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            GCGCGCAGAGAGGGAGTGGGCAA 143
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         "USF"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Location/Qualifiers
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Adeno associated virus serotype 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Example 2; Fig 2; 108pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         BP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AAD00772 standard; DNA; 4718
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    .226
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           vaccine; transgene; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               misc_feature
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             protein_bind
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AAD00772;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      61
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Job time : 66.9124 secs
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              adeno-associated virus; AAV; cytostatic; antipsoriatic; antirheumatic; antiarhitit; neuroprotective; antidabelic; antithritid; dermatological; antiinflammatory; gene therapy; vaccine; hyperproliferative; cancer; psoriasis; autoimmune disease;
                                                                                                                                                                                                                                                                                                                                                                                                                                           Gaps
                                                                                P-PSDB; AAY71161, AAY71164, AAY71165, AAY71166, AAY71167, AAY71168,
                                                                                                                         Novel adeno-associated virus serotype 1 polynucleotide useful for preparation of medicament for delivery of a transgene to a host.
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                                                                                                                                                                                                                                                                                                                                                                                  Sequence 4718 BP; 1121 A; 1393 C; 1273 G; 931 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                            Length 4718;
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83.24; Score 119; DB 3; Length 47.
Best Local Similarity 89.54; Pred. No. 7.2e-22;
Matches 128; Conservative 0; Mismatches 15; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 121 GCGCGCAGAGAGGGAGTGGGCAA 143
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                                                                                                                                                                   Claim 1, Fig 1, 108pp; English.
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           (UYPE-) UNIV PENNSYLVANIA
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                                       Wilson JM, Xiao W;
                                                                   WPI; 2000-376571/32
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The invention relates to a novel method for detecting adeno-associated virus (AAV) sequences in a sample, which comprises subjecting a sample containing a DNA to amplification via a polymerase chain reaction (PCR). The AAV sequence have the following activities: cytostatic, antithyoriatic, antithyorid, dermatological, and antiinflammatory. The AAV sequence can be used in gene therapy or as part of a vaccine to treat disorders. The method is useful in detecting and/or identifying AAV sequences and isolating novel sequences that are identified. The sequences may be used e.g. for preventing or treating hyperproliferative conditions such as cancers and psoriasis and other autoimmune diseases like rheumatoid arthritis, multiple sclerosis, diabetes, autoimmune thyroiditis, scleroderma or Crohn's disease. This polynucleotide sequence represents an AAV related DNA sequence of the invention.
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                                                                                                                                                                                                                                                                                         Detecting adeno-associated virus sequences in a sample, useful for preventing or treating hyperproliferative or autoimmune diseases, comprises subjecting a sample having a DNA to amplification via
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89.5%; Pred. No. 7.2e-22;
iive 0; Mismatches 15;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Claim 14; SEQ ID NO 6; 419pp; English.
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                                                                                                                                                                 Alvira M;
01-MAY-2002; 2002US-0377066P.
05-JUN-2002; 2002US-0386675P.
                                                                                                                                                                                                                                                                                                                                                                                                   polymerase chain reaction.
                                                                                            (UYPE-) UNIV PENNSYLVANIA.
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Matches 128; Conservative
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OM nucleic

Run on:

Sequence:

Searched:

Database

Result No.

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AAV-1
1P 2002529098-A/1
10-SEP-2002
02-NOV-1999 JP 2000581227
02-NOV-1998 US 60/107114
JAAES M WILSON WEIDONG XIAO
CIZNIS/09,A61K31/711,A61K48/00,A61P43/00,C12N1/15,C12N1/19, PC
                                                                                                                                                                      AM2021525 Adeno-a880c
AM014135 Sequence
BD218219 Adeno-a88
116806 Sequence 1
AR223306 Sequence
AX106702 Sequence
AX4400 Sequence
AX440199 Sequence
AX703496 Sequence
BD218218 Adeno-a88
AX703496 Sequence
AX703496 Sequence
AX106701 Sequence
                                                                                 AF513851 Adeno-ass
BD242774 Adeno-ass
AR562506 Sequence
AR140333 Sequence
AX286293 Sequence
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JP 2002529098-A/1.
unidentified
unidentified
unclassified.
l (bases I to 4718)
Wilson, J.M. and Xiao, W.
Adeno-associated virus serum type 1 nucleic acid sequence, vector and host call containing the same
Patent: JP 2005259098-A 1 10-SEP-2002;
THE TRUSTEES OF THE UNIVERSITY OF PENNSYLVANIA
                            CQ972062 Sequence
CS073592 Sequence
AX753246 Sequence
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(2223). .(4430)
Location/Qualifiers
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/organism="unidentified"
/mol_type="genomic DNA"
/db_xref="taxon:32644"
                                                   CS073592
AX753246
AF513851
BD242774
AR562506
AR140333
                                                                                                                                                                                               AR034135
BD218219
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AR223306
AR523306
AX106702
A46400
AX418199
AX703496
BAX703496
BAX23308
AR6583388
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BD094552
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AX286292
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AA2LTR2
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Best Local Similarity
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DEFINITION
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KEYWORDS
SOURCE
ORGANISM
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TITLE
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C0972062 Sequence
CS073252 Sequence
AK753246 Sequence
AK7532813851 Adeno-ass
AF028704 Adeno-ass
BD242775 Adeno-ass
BD242776 Adeno-ass
AK562507 Sequence
AK753251 Sequence
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AF028704 Adeno-ass
BD242775 Adeno-ass
AR562507 Sequence
                                                                                                                         November 28, 2005, 12:51:27; Search time 522.566 Seconds (without alignments) 15555.198 Million cell updates/sec
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AR562498 Sequence
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                                                                                                                                                                                                                                     ttacccctagtgatggagtt............gcagagagagtgggcaa 143
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                                                                                                                                                                                                                                                                                                                                                                  11766282
                    GenCore version 5.1.6 (c) 1993 - 2005 Compugen Ltd.
                                                                                                                                                                                                                                                                                                                            5883141 segs, 28421725653 residues
                                                                                                                                                                                                                                                                                                                                                               Total number of hits satisfying chosen parameters:
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Maximum Match 100%
Listing first 45 summaries
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AF063497
CQ972062
CS073592
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AF028704
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AR562507
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AR562498
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Gapop 10.0 , Gapext 1.0
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Maximum DB seq length: 2000000000
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9b_pr: * . *
9b_er: *
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Mison, Am. and Xiao, W.
Adeno-associated virus serotype 1 nucleic acid sequences, vectors
and host cells containing same
Patent: US 6759237-A 1 06-UUL-2004;
The Trustees of the University of Pennsylvania; Philadelphia, PA
Location/Qualifiers
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Adeno-associated virus 1
Viruses; ssDNA viruses; Parvoviridae; Parvovirinae; Dependovirus.
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Sequence 1 from patent US 6759237.
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Sequence 6 from Patent EP1310571.
AX753251 GI:32166108
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/mol_type="genomic DNA"
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LNLIEGAPLTVAEKLORDFLVQWRRYSKAPBALFPYQFEKGESYFHLHILVETTGWKS
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Lyppgykyldgoppageprnaadbalehdkydgolkagdnylaktryhadbarge
Rlogdpasegallaryvgakkkuleplolyeggarrapgkkrapyggspgepsssgig
Krigopakkklinfgorgdsesypdpoploepatpaavgpttmasgagapmadnnega
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Adeno-associated virus 1
Viruses; ssDNA viruses; Parvoviridae; Parvovirinae; Dependovirus.
1 (bases 1 to 4718)
Xiao, W., Chirmule, N., Berta, S.C., McCullough, B., Gao, G. and Wilson, J.M.
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Xiao, W. and Wilson, J. M.
Direct (Submission
Submitted (05-MAY-1998) IHGT, University of Pennsylvania, 3601
Spruce Street, Philadelphia, PA 19104, USA
Location/Qualifiers
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/db_xref="taxon:85106"
/note="AAV1"
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                                                                                                                                                                                  Match 100.0%; Score 143; DB 6; Local Similarity 100.0%; Pred. No. 1.8e-21; es 143; Conservative 0; Mismatches 0;
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/protein_id="AAD27758.1"
/db_xref="GI:4689098"
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/mol_type="unassigned DNA"
/db_xref="taxon:85106"
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PAT 23-JUN-2003
                                                                                    Wilson, J.M., Gao, G., Alvira, M.R. and Vandenberghe, L.H.
Adeno-associated virus (aav) clades, sequences, vectors containing
same, and uses therefor
Patent: WO 200503331-A 180 14-APR-2005;
The Trustees of the University of Pennsylvania (US)
Location/Qualifiers
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/noTe="adeno-associated virus serotype 7"
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    .6xganishal-Adeno-associated virus /mol type-"unassigned DNA"
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Sequence 1 from Patent EP1310571.
AX753246
                                                                                                                                                                                           /organism="unidentified"
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NNLTGTVQYSEDSEYQLPYLGSAHQGCLPPPRDDVPMIPOYOYLTLANGSQAVGRSS
YCLEYPPSQMLRTGNNFTSYTFEBPPPHSSYAHSQSLDRLAMPLIDQVLYYLANTQ
NQSGSAQNKDLLFSRGSPAGMSVQPKNWLPGFCYRQORVSKTKTDNNNSNPTWTGASK
YNLNGRESIINPGTAMASHKDDEDKFFPMSGVMIFGKESAGASNTALDNVMITDEEEI
                                                                                       KATNPVATERFGTVAVNFOSSSTDPATGDVHAMGALPGMVWQDRDVYLGGPIMAKIPH
TDGHFHPSPLMGGFGLKNPPPQILIKNTPVPANPPAEFSATKFASFITQYSTGQVSVE
IEWELQKENSKRWNPEVQYTSNYAKSANVDFTVDNNGLYTEPRPIGTRYLTRPL"
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Methods and compositions for lowering total cholesterol levels and treatment of heart disease
Patent: WO 2004109922-A 7 16-DEC-2004;
The Trustees of The University of Pennsylvania (US)
Location/Qualifiers
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   DGVGNASGNWHCDSTWLGDRVITTSTRTWALPTYNNHLYKQISSASTGASNDNHYFGY
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/mol_type="unassigned DNA"
/db_xref="taxon:272636"
                                                                                                                                                                  Query Match 100.0%; Score 143; DB 13;
Best Local Similarity 100.0%; Pred. No. 1.8e-21;
Matches 143; Conservative 0; Mismatches 0;
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larity 97.2%; Pred. No. 7.2e-20;
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Sequence 7 from Patent WO2004108922.
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LILIEQAPLYVAEKLQRDFLVQMRNVSKAPEALFFVQPEKGBSFFHLHVLVETTGVKS
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TQPELQMAWTRMEET YRAVEPTLPRINGAUGHLTHVSGTOGONKENLAPNSDAPVIRS
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TRRLEHDFGKVTKQEVKEFFRWASDHVTEVAHEFFVNKGGASKRPAPDDADISEPKRA
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LVLPGYKYLG9FNGLDKGEPVNAADAALEHDKAYDQQLKAGDNPYLRYNHADAEFQE
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GKKGQQPARKRLNFGQTGDSBSVPDPQPLGEPPAAPSSVGSGTVAAGGGAPMADNNBG
ADGVGNASGGNHCDSFWLGDRVITTSFRTWALLPTYNNILYKQLSSETAGSTNDNYTYFG
YSTPWGYFDPNRFHCHFSPRDWQRLINNNWGPRPKKLRFKLFRIQVKSVTTNDGVTTI
ANNITYSTIQYPRDSPRYQLPYLGSAHQGCLPPPPADVPHIPQYGYLTLINNGSQSVGRS
SFYCLEYFPSQMLRTGNNFEFSYSFEDVPFHSSYAHSQSLDRLMNPLIDQYLYYLART
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TKYHLNGRNSLVNPGVAMATHKDDEDRFFPSSGVLI FGKTGATNKTTLENVLMTNEEE
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HTDGNFHPSPLMGGFGLKHPPPQILIKNTPVPANPPEVFTPAKFASFITQYSTGQVSV
EIEWELQKENSKRMNPEIQYTSNFEKQTGVDFAVDSQGVYSEPRPIGTRYLTRNL"
                                         VRL 05-SEP-2002
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RDCLECFPGVSESQPVVRKKTYRKLCAIHHLLGRAPEIACSACDLVNVDLDDCVSEQ"
  Adeno-associated virus 7 nonstructural protein and capsid protein genes, complete cds.
AF513851
AF513851.1 GI:22652859
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Submitted (20-MAY-2002) Institute for Human Gene Therapy, University of Fennsylvania, M6.40 Maloney Bldg, 36th & Spruce Sts, Philadelphia, PA 19104, USA Location/Qualifiers
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Adeno-associated virus 7
Viruses; ssDNA viruses; Parvoviridae; Parvovirinae; Dependovirus.
1 (bases 1 to 4721)
20, G.P., Alvira,M.R., Wang,L., Calcedo,R., Johnston,J. and
                                                                                                                                                                                                                                                                                                                             Novel adeno-associated viruses from rhesus monkeys as vectors for
                                                                                                                                                                                                                                                                                                                                            human gene therapy
Proc. Natl. Acad. Sci. U.S.A. 99 (18), 11854-11859 (2002)
12192090
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/note="similar to AAV2 VP1 protein"
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|mol_type="genomic DNA"
|specific host="thesus monkey"
|db_xref="taxon:202812"
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KYSARYMELVGMLVDRGITSBKCMTGEDQASY IS FNAASNERS GIKKALDNAGKIMAL
TKSARYMELVGMLVDRGITSBKCMTGEDQASY IS FNAASNERS GIKKALDNAGKIMAL
TKSARYMENT VRILELINGYDPAYAGSVFLGMAQKRFGKRYTIMLFG
PATTGKTVI KAEJ IAPAVPFYCKOVNYNEN PF PNDCVDKMY I WWEEGACMTAKVVESAKA
I LGGSKVRVDQKCKSSAQIDPTPVI YTSNTNMCAV I DGNSTT FEHQOPLQDRMFKFEL
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TRALBHDFGKTYGGVERVDFADRY QDNCSRHAGMLQNLFFFEL
TRALBHDFGFADDADKSEPKRADHYTEVAHEFFYNKGGANKRPAPDDADKSEPKRA
TRACSTADFSTSDAEGARVDFADRY QDNCSRHAGMLQNLFFCKTCERNAQNFNI CFTHGT
RDCSECFFGVSESQPVVRKRTYRKLCAIHHLLGRAAPEIACSACDLVNVDLDDCVSEQ
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RLQEDTSFGGNLGRAVFQAKKRVLEPFGLVEEGAKTAPGKKRPVEGSPQEPDSSSGIG
KRQQPAKKRLNFGGTGDSBSVPDPQPLGEPPATPANGFTTWASGGGAPMADNNEGA
DGVGNASGNWHCDSTWLGNYITTSTRTWALPTYNHLYKQISSASTGASNDNHYFGY
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NNLTSTVQVFSDSEYQLPYVLGSAHQGCLPPFPADVFMIPQYGYLTLNNGSQAVGRSS
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LNLIEQAPLTVAEKLORDFLVQMRRVSKAPEALFFVQFEKGESYFHLHILVETTGVKS
MVLGRFLSQIRDKLVQTIYRGIEPTLPNMFAVTKTRNGAGGGNKVVDECYIPNYLLPK
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Adeno-associated virus 6
Adeno-associated virus 6
Viruses; BaDNA viruses; Parvoviridae; Parvovirinae; Dependovirus.
(Dases 1 to 4683)
Rutledge, B.A., Halbert, C.L. and Russell, D.W.
Infectious clones and vectors derived from adeno-associated virus (AAV) serotypes other than AAV type 2
Virol. 72 (1), 309-319 (1998)
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Rutledge B.A. and Russell, D.W.
Direct Submission
Submitted (24-SPB-1997) Hematology, Univ. of Washington, Box 357720, Seattle, WA 98195, USA
Location/Qualifiers
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/organism="Adeno-associated virus 6"
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AF028704
97.2%; Pred. No. 7.2e-20; ive 0; Mismatches 4
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product="capsid protein VP1"
/protein id="AAB95450.1"
/db_xrefg="GI:2766607"
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   Best Local Similarity 97.2
Matches 138; Conservative
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Query Match

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Adeno-associated virus serum type 1 nucleic acid sequence, vector and host cell containing the same.
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JAMES M WILSON, WEIDONG XIAO
CI2N15/09, A61K31/711, A61K48/00, A61P43/00, C12N1/15, C12N1/19, PC
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Wilson,J.M. and Xiao,W.
Adeno-associated virus serotype 1 nucleic acid sequences, vectors and host cells containing same
Patent: US 6759237-A 19 06-JUL-2004;
The Trustees of the University of Pennsylvania; Philadelphia, PA
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Wilson,J.M. and Xiao,W.
Walson,J.M. and Xiao,W.
Adeno-associated virus serum type 1 nucleic acid sequence, vector and host cell containing the same
Patent: JP 2002529098-A 1 10-SEP-2002;
THE TRUSTEES OF THE UNIVERSITY OF PENNSYLVANIA
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C12N5/10,C12P21/02//A61K35/76,C12N15/00,C12N5/00
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Pred. No. 1.6e-16;
0; Mismatches 3;
                                                                                                                                                 DNA
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Sequence 19 from patent US 6759237.
AR562507
                                                                                                                                                                                                                                                                                                                                                                               /organism="unknown"
/mol_type="genomic DNA"
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05-NOV-1998 US 60/10711
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JP 2002529098-A/1.
unidentified
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10-SEP-2002
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Best Local Similarity 97.6%;
Matches 122; Conservative
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AR562507/c
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NQSGSAQNKDLLFSRGSPAGMSVQPKNWLPGPCYRQQRVSKTKTDNNNSNFTWTGASK
YNLNGRESIINPGTAMASHKDDKDKFPPMSGWAIFGKESAGASNTALDNWITDEEEI
KATNPVATERGTVAVNIGOSIIPPROTOVHVMGALFGMWWQDBVYLCQPINAKIPH
TDGHPHSPLMGGGLKHPPPQIINKTPVPANPAESATKRASFITQYSTGQYSVB
IEWELQKENSKRWNPEVQYTSNYAKSANVDFTVDNNGLYTEPRPIGTRYLFPL"
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                                                                                                                    Score 121.8; DB 13; Length 4683;
Pred. No. 7.1e-17;
0; Mismatches 2; Indels 0;
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Wilson,J.M. and Xiao,W.
Adeno-associated virus serum type 1 nucleic acid and host cell containing the same
Patent: JP 200529098-A 10 10-SEP-2002;
THE TRUSTEES OF THE UNIVERSITY OF PENNSYLVANIA
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Pred. No. 1.6e-16;
); Mismatches 3;
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Key Location/Qualifiers
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Location/Qualifiers
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10-SEP-2002
02-NOV-1999 UP 50/107114
JAMES M WILSON, WEIDONG XIAO
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JP 2002529098-A/10.
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llarity 97.6%;
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ilarity 98.4%;
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les 123; Conserv
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TOPELOWAWTRNEEYISACLANLAERKRLVAQHLTHVSQTQEQONKENLAPNSDAPVIRS
KTSARYMELVGWLVDRGITSEKQWIQEDQASYISFNAASNSRSQIKAALDNAGKIMAL
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Xiao, W., Chirmule, N., Berta, S.C., McCullough, B., Gao, G. and Wilson, J.M.
                                                               Adeno-associated virus 1
Viruses; ssDNA viruses; Parvoviridae; Parvovirinae; Dependovirus.
                                                                                                            Gao,G., Wilson,J.M. and Alvira,M.
A method of detecting and/or identifying adeno-associated virus
(AVV) sequences and isolating novel sequences identified thereby
Patent: EP 1310571-A 6 14-MAY-2003;
The Trustees of The University of Pennsylvania (US)
Location/Qualifiers
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Submitted (OS-MAY-1998) IHGT, University of Pennsylvania, 3601
Spruce Street, Philadelphia, PA 19104, USA
Location/Qualifiers
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10196295
                                                                                                                                                                                                                                                                                                         Length 4718;
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Pred. No. 2.9e-16;
0; Mismatches 15; Indels
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/mol_type="genomic DNA"
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                                                                                                                                                                                                           1. .4718
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Adeno-associated virus 1, complete genome.
AF063497
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Adeno-associated virus 1
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Xiao, W. and Wilson, J.M.
 AX753251
AX753251.1 GI:32166108
                                                  Adeno-associated virus
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Best Local Similarity 89.5%;
Matches 128; Conservative (
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AF063497/c
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Mison, Am. and Xiso, W.
Adeno-associated virus serotype 1 nucleic acid sequences, vectors
and host calls containing same
Patent: US 6759237-A 1 06-UUL-2004;
The Trustees of the University of Pennsylvania; Philadelphia, PA
Location/Qualifiers
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   Adeno-associated virus serum type 1 nucleic acid sequence,
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Best Local Similarity 89.5%; Pred. No. 2.9e-16;
Matches 128; Conservative 0; Mismatches 15; Indels
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(2223). .(4430).
Location/Qualifiers
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AR562498 47562498.1 GI:53976564
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/mol_type="genomic DNA"
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Sequence 6 from Patent EP1310571.
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                  vector and host
cell containing the same
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Matches 128; Conserv
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PATTGKTYATABALIHAVPPYGCVNWTWENEPRPNDVUDKUTWWEGRATAKVRAKA

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2223. .4433

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Ses

Query Match 83.2%; Score 119; DB 13; Length 4718;
Best Local Similarity 89.5%; Pred. No. 2.9e-16;
Matches 128; Conservative 0; Mismatches 15; Indels 0; Gaps 0;
Oy 1 Traccccradrearracyccacreccreccreccyccrecccrecccc

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8 6 8 6 8

 Search completed: November 29, 2005, 00:05:26 Job time : 523.566 secs



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November 28, 2005, 18:24:29; Search time 454.049 Seconds (without alignments) 14735.325 Million cell updates/sec
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143
1 ttacccctagtgatggagtt......cgcagagagggagtgggcaa 143
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GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.
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Maximum Match 100%
Listing first 45 summaries
                                                                  OM nucleic - nucleic search, using sw model
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Gapop 10.0 , Gapext 1.0
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9D_est2::*
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9D_est4::*
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9D_est7::*
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                                                                                                    Run on:
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No. Score Match Length DB ID Description

C 1 37.8 26.4 763 2 BG490707 BG490707 602520211

C 2 37.8 26.4 1021 5 BG38990 BG338990 AGENCOURT

C 3 37.4 26.2 644 2 BB632576 BB632576 BB632576

C 4 36.2 25.3 1021 5 BU338990 CV352119 BG38990 AGENCOURT

C 3 6 2 2 3 3 2 1 C 1021 5 BU338990 CV352119 BG51469 BG51469

C 10 35.6 24.9 578 2 BB651469 BB651469

	C 23 34 24 34 26 25 34 26 34 29 34 31 3	644.4.4.4.4.4.4.4.4.4.4.4.4.4.4.4.4.4.4	671 10 6890 10 3 899 10 3 4 8 8 8 8 8 8 8 8 8 8 8 8 8 8 8 8 8 6 6 1 3 4 3 8 8 6 6 1 2 8 8 6 6 1 2 8 8 6 6 1 2 8 8 6 6 1 2 8 8 6 6 1 2 8 8 6 6 1 2 8 8 6 6 1 2 8 8 6 6 1 2 8 8 6 6 1 2 8 8 6 6 1 2 8 8 6 6 1 2 8 8 6 6 1 2 8 8 6 6 1 2 8 8 6 6 1 2 8 8 6 6 1 3 4 4 5 8 6 6 1 3 4 6 6 6 6 1 3 4 6 6 6 6 1 3 4 6 6 6 6 1 3 4 6 6 6 6 1 3 4 6 6 6 6 6 6 6 6 6 6 6 6 6 6 6 6 6 6	14 24.1 671 10 CW914921 CW914921 CW914921 RPCI42_15 14 24.1 890 10 AG127787 AG127787 BAG127787 BAG12787 BAG1278
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Eukaryota, Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi; Muroidea; Murinae; Mus.

1 (bases 1 to 644)

2 Arakawa, T., Carninci, P., Fukuda, S., Furuno, M., Hanagaki, T., Hara, A., Hiramoto, K., Hori, F., Ishii, Y., Ito, M., Kawai, J., Kohno, M., Okazaki, Y., Okido, T., Saito, R., Sakai, C., Sakai, K., Sano, H., Sasaki, D., Shibata, K., Shinagawa, A., Shiraki, T., Takeda, Y., Tanaka, T., Toya, T., Muramatsu, M. and Hayashizaki, Y. RIKEN Mouse ESTS (Arakawa, T., Muramatsu, M. and Hayashizaki, Y. Inpublished (2001)
                                                                                                                                                                                                         BB632576 RIKEN full-length enriched, adult male hypothalamus Mus musculus cDNA clone A230067815 5', mRNA sequence.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Context: Yoshhiide Hayashizaki
Laboratory for Genome Exploration Research Group, RIKEN Genomic
Sciences Center(GSC), Yokohama Institute
The Institute of Physical and Chemical Research (RIKEN)
1-7-22 Suehiro-cho, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan
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Fax: 81-45-503-9222
Email: genome-reagags.riken.jp, URL:http://genome.gas.riken.jp/
Carninci.p., Shibata,Y., Hayatsu,N., Sugahara,Y., Shibata,Y.,
Itoh,M., Konno,H., Okazaki,Y., Muramatsu,M. and Hayashizaki,Y.
Normalization and subtraction of cap-trapper-selected cDNAs to prepare full-length cDNA libraries for rapid discovery of new genes. Genome Res. 10 (10), 1617-1630 (2000)
wagi,K., Fujiwake,S., Inoue,K., Togawa,Y., Izawa,M., Ohara,E., Matsuiki,M., Yoneda,Y., Ishikawa,T., Ozawa,K., Tanaka,T.,
and Hayashizaki,Y.
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Computational Analysis of Full-Length Mouse cDNAs Compared with
Human Genome Sequences. Mamm. Genome. 12, 673-677 (2001)
Please visit our web site (http://genome.gsc.riken.go.jp) for
further details.
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prepared and sequenced in Mouse Genome Encyclopedia
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|lab_host="DH10B"
'clone_lib="RIKEN full-length enriched, adult male
tissue_type="hypothalamus"
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/organism="Mus musculus"
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db_xref="taxon:10090"
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Context: Robert Strausberg, Ph.D.

Fmail: cgapbs-r@mail.nh.gov

Tissue Procurement: DCTD/DTP

CDNA Library Preparation: Rubin Laboratory

CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)

DNA Sequencing by: Agencourt Bioscience Corporation

Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:

http://image.llnl.gov

Plate: L.C.M.2413 row: p column: 02

High quality sequence start: 36

High quality sequence stop: 231.
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                                                                                                                                                                                                                                                26 CTCCCTCTCTGCGCGCTCGCTCGCTCGGTGGGGCCTGCGGACCAAAGGTCCGCAGACGGC 85
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Mammalia, Eutheria, Euarchontoglires, Primates, Catarrhini,
                                                                                                                                                                                                                                                                                                                  261 GGCCTGCGCTGCCCGGCGCTCGCTCTGCCCTGCCCGCCTCGCTTCGCTC
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1 (bases 1 to 1021)

NIH-MGC http://mgc.ncl.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished (1999)
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                                                                              26.4%; Score 37.8; DB 2; Length 763; 58.4%; Pred. No. 13;
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Direct Submitted (02-JUN-1999) Genoscope - Centre National de Sequencage : Submitted (02-JUN-1999) Genoscope - Centre National de Sequencage : BP 191 91006 EVRY cedex - FRANCE (E-mail : seqref@genoscope.cns.fr - Web : www.genoscope.cns.fr)

Determination of this BAC-ens.fr)

Determination of this BAC-ens sequence was carried out as part of a collaboration with the Berkeley Drosophila Genome Project (BDGP). The BDGP is constructing a physical map of the Drosophila melanogaster BAC library was prepared by Kazutcoy Ososophila melanogaster BAC library was prepared by Kazutcoy Ososophila Aaron Mammoser in Pieter de Jong's laboratory in the Department of Cancer Genetics at the Roswell Park Cancer Institute in Buffalo, NY. The library is named RPCI-98 and was constructed by partial EcoRI digestion of Drosophila Dhy provided by the BDGP From the isogenic strain y2; cn bw sp, the same strain used for the BDGP's pland by the corder individual BAC clones, the entire library and how to order individual BAC clones, the entire library or filters for hybridization from the BACPAC Resource Center can be found at http://Dacpac.med.buffalo.edu/drosophila_bac.htm.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CNS0072Q 932 bp DNA linear GSS 03-JUN-1999
Drosophila melanogaster genome survey sequence T7 end of BAC #
BACR14B09 of RPCI-98 library from Drosophila melanogaster (fruit
  pBluescript II SK- plasmids were excised from the lambda bage in the state of the plant of the plant of the page. The library was normalized using method 4 described in Bonaldo et al (1996) Genome Research 6: 791-806.
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                                                                                                                                                                                                                                                                                                16 GAGTTGCCCACTCCCTCTGCGCGCTCGCTCGGTGGGGCCTGCGGACCAAAGGTC
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Bukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
Ephydroidea; Drosophilidae; Drosophila.
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                                                                                                                                                       Length 604;
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                                                                                                                                                       DB 3;
                                                                                                                                                     Score 36.2; DB; Pred. No. 34; 0; Mismatches
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36.3%; Pred. No. 34;
:ive 32; Mismatches
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/db_xref="taxon:7227"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     fly), genomic survey sequence.
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/clone lib="RPCI-98"
/note="end : T7"
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                                                                                                                                                     25.3%;
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Anote="Vector: pBluescript II SK-; Site_1: EcoRI; Site_2: XhoI; This library, constructed by John Davies and Jeffrey McDermott, combines DNNs from CC-1690 cells grown to mid-log phase in TAP (acetate-containing) medium in the light, TAP medium in the dark, HS (minimal) medium in the ambient levels of CO2 and HS medium bubbled with 5% CO2. Poly mRNA was purified from each sample, pooled and CDNA synthesized. The CDNA was directionally cloned into lambda ZAP II (Stratagene) in the ECORI (5') and XhoI (3') sites.
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/clone lib="C. reinhardtii CC-1690, normalized, Lambda Zap
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1024113H09.yl C. reinhardtii CC-1690, normalized, Lambda Zap II
Chlamydomonas reinhardtii cDNA, mRNA sequence.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Bukaryota; Viridiplantae; Chlorophyta; Chlorophyceae; Chlamydomonadales; Chlamydomonadaceae; Chlamydomonadaceae; Chlamydomonadaceae; Chlamydomonaes 1 to 604)
Grossman, A., Chang, C.-W., Davies, J., Harris, E., Hauser, C., Edebure, P., McDermott, J. P., Shrager, J., Silflow, C. and Stern, D. Analyees of the Chlamydomonas reinhardtii Genome: A Model, Unicellular System for Analyzing Gene Function and Regulation in
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                         Score 37.4; DB 2; Length 644; Pred. No. 16; 0; Mismatches 31; Indels (
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/strain="CC-1690 wild type mt+
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Vascular Plants. Project: 1024b
Unpublished (2001)
Contact: Charles Hauser
Cornact: Charles Hauser
DCMB Box 91000
Duke University
Durham, WC 27708-1000
Tel: 919 613 8159
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           89 GCTCTGCTCTGCCGGCCCCACCGAGCG 115
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    595 CTCTACTTTGACGTGCCCCCCGCGTG 621
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Chlamydomonas reinhardtii
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                                                                                                                                                                                                                                                                                                                                                                                                                           ch 26.2%;
1 Similarity 64.4%;
56; Conservative (
                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match
Best Local Similarity
Matches 56; Conserv
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/organizami-mission Saptems
/ob_xref="taxon:9606"
/db_xref="taxon:9606"
/db_yref="taxon:9606"
/db_yref="taxon:
                                                                                                         Hominidae, Homo.

1 (Dasea I to 318)

Dias Neto, E., Garcia Correa, R., Verjovski-Almeida, S., Briones, M.R.,

Nagai, M.A., da Silva, W. Jr., Zago, M.A., Bordin, S., Costa, F.F.,

Goldman, G.H., Carvalho, A.F., Matsukuma, A., Baia, G.S., Simpson, D.H.,

Brunstein, A., deoliveira, P.S., Bucher, P., Jongeneel, C.V.,

O'Hare, M.J., Soares, F., Brentani, R.R., Reis, L.F., de Souza, S.J. and

Simpson, A.J.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SAIL_781_802.v2 SAIL Collection Arabidopsis thaliana genomic clone CL507458
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Eax: +55-11-2707001
Email: asimpson@ludwig.org.br
This sequence was derived from the FAPESP/LICR Human Cancer Genome
Project. http://www.ludwig.org.br.
Location/Qualifiers
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Arabidopsis thaliana
Eukaryota, Viridiplantae, Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons;
rosids; eurosids II; Brassicales; Brassicaceae; Arabidopsis.
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Sessions, A., Burke, E., Presting, G., Aux, G., McElver, J., Patton, D.,
Dietrich, B., Ho, P., Bacwaden, J., Ko, C., Clarke, J.D., Cotton, D.,
Bullis, D., Snell, J., Miguel, T., Hutchison, D., Kimmerly, B.,
Mitzel, T., Katagiri, F., Glazebrook, J., Law, M. and Goff, S. A.
A high-throughput Arabidopsis reverse genetics system
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Chordata; Craniata; Vertebrata; Euteleostomi;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Contact: Simpson A.J.G.
Laboratory of Cancer Genetics
Ludwig Institute for Cancer Research
Rua Prof. Antonio Prudente 109, 4 andar, 01509-010, Sao Paulo-SP,
                                                                                                                                                                                                                                                                                                                                                                                               Shotgun sequencing of the human transcriptome with ORF expressed sequence tags
Proc. Natl. Acad. Sci. U.S.A. 97 (7), 3491-3496 (2000)
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                                     Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, suceseu
Mammalla, Eutheria, Euarchontoglires, Primates, Catarrhini,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /organism="Homo sapiens"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Tel: +55-11-2704922
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MR3-GN0187-201100-010-f10 GN0187 Homo sapiens CDNA, mRNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Manualia; butneria; buarchonicogilres; Frimates; Catairnin; Manualia; butneria; buarchonicogilres; Frimates; Catairnin; Mominidae; Homo.

S NIH-MGC http://mgc.nci.nih.gov/.

In (brown Institutes of Health, Mammalian Gene Collection (MGC)

Contact: Robers Erauaberg, Ph.D.

Contact: Robers Erauaped by: The I.M.A.G.E. Consortium (LLNL)

DNA Sequencing by: Agencourt Bioscience Corporation

Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at:

http://image.llnl.gov

Plate: LLCM2413 row: p column: 02

High quality sequence start: 36

High quality sequence stop: 231.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Bukaryoča, Metazoa; Chordata; Craniata; Vertebrata, Buteleostomi;
Mammalla; Butherla; Buarchontoglires; Primates; Catarrhini;
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Matches 65; Conserv
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genes. Genome Res. . 10 (10), 1617-1630 (2000)

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wathiki, M., Yoneda, Y., Ishikawa, T., Ozawa, K., Tanaka, T.,
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Hayashizaki, Y.
Computational Analysis of Full-Length Mouse cDNAs compared with
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               BI905802 793 bp mRNA linear EST 16-OCT-2001
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CCTCTCTGCGCGCTCGCTCGGTGGGGCCTGCGGACCAAAGGTCCGCAGACGGCAGA 88
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/dev stage="0 day neonate"
/lab_host="DH10B"
/clone_lib=RIKEN full-length enriched, 0 day neonate
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Human Genome Sequences. Mamm. Genome. 12, 673-677 (2001)
Please visit our web site (http://genome.gsc.riken.go.jp) for
further details.
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Pred. No. 49;
0; Mismatches
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/db_xref="taxon:10090"
/clone="C230083H05"
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Arakawa, T., Carninci, P., Fukuda, S., Furuno, M., Hanagaki, T., Korno, H., Konda, M., Koya, S., Matsuyama, T., Miyazaki, A., Nomura, K., Ohno, M., Okazaki, Y., Kokao, T., Miyazaki, T., Sano, H., Sasaki, C., Sakai, K., Sano, H., Sasaki, D., Shibata, K., Shinagawa, A., Shiraki, T., Tagami, M., Tagawa, A., Takahashi, F., Takeda, Y., Tanaka, T., Toya, T., Muramatsu, M. and Hayashizaki, Y. RIKEN Mouse ESTS (Arakawa, T., et al. 2001)
                                                                        Applied Trait Genetics
Syngenta Biotechnology Inc.
Syngenta Biotechnology Inc.
Syngenta Biotechnology Inc.
Syngenta Arabidopsis Insertion Library (SAIL) lines are available through the Arabidopsis Biotogical Resource Center (ARKC).
Sequences represent a pool of amplified genomic regions and not single contiguous sequences.
Class: TDNA tagged.
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Laboratory for Genome Exploration Research Group, RIKEN Genomic
Sciences Center(GSC), Yokohama Institute
The Institute of Physical and Chemical Research (RIKEN)
1-7-22 Suehiro-cho, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan
Tel: 81-45-503-922
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                31 TCTCTGCGCCTCGCTCGCTCGCTGGGGCCTGCGAAAGTCCGCAGACGCAGAGG 90
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Carninci.P., Shibata,Y., Hayatsu,N., Sugahara,Y., Shibata,K.,
Itoh,M., Konno,H., Okazaki,Y., Muramatsu,M. and Hayashizaki,Y.
Normalization and subtraction of cap-trapper selected cDNAs to
prepare full-length cDNA libraries for rapid discovery of new
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      organism="Arabidopsis thaliana"
                      Plant Cell 14 (12), 2985-2994 (2002)
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Matches 64; Conservative
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Gaps ö

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Contact: Robert Strausberg, Ph.D.
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/mol_type="mRNA"
/mol_type="mRNA"
/db_txef="taxon:9606"
/clone="InAGE:5212016"
/clone=lib="NIH_MGC_118"
/clone=lib="NIH_M
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Mammalia, Eutheria, Euarchontoglires, Primates, Catarrhini,
                          Eukaryota, Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalla; Butheria; Euarchontoglires; Primates; Catarrhini;
                                                                                                                                                                                         Unpublished (1999)
Contact: Robert Strausberg, Ph.D.
Email: Gapbs-remail.nih.gov.
Tissue Procurement: Life Technologies, Inc.
CDNA Library Preparation: Life Technologies, Inc.
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Thoyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov.
Plate: LlaMn1532 row: e column: 09
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1 (bases 1 to 1115)
NIH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished (1999)
                                                                                                        1 (bases 1 to 793)
NIH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
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Location/Qualifiers
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Homo sapiens
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/US xref="taxon:9606"
/ (UD xref="taxon:9606"
/ (Lone="IMARRS:5724802"
/ (Lone="IMARRS:5724802"
/ (Lone="IMARRS:5724802"
/ (Lone="IMARRS:5724802"
/ (Lone="Organ: Ovary" (Dool of 3); Vector: DCMV-SPORT6;
/ (Lone="Organ: Ovaries, from females ranging in age from 38 to of three ovaries, from females ranging in age from 38 to of 100 to 1
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Totoki, Y., Watanabe, H. and Sakaki, Y.
Direct Submission
Submitted (102-M012-2001) Asao Fujiyama, The Institute of Physical
and Chemical Research (RIKEN), Genomic Sciences Center (GSC);
1-7-22 Suehiro-chou, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan (R-mail:chimpbes@gsc.riken.go.jp, URL:http://hgp.gsc.riken.go.jp/,
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Pan troglodytes DNA, clone: PTB-076K10.R, genomic survey sequence.
Email: cgapbs-remail.nih.gov
Tissue Procurement: Invitrogen
cDNA Library Preparation: Life Technologies, Inc.
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Agencourt Bioscience Corporation
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: LLAM12714 row: k column: 11
High quality sequence state: 9
High quality sequence stop: 691.
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Mammalia; Butheria; Buarchontoglires; Primates; Catarrhini;
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Gaps

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/tissue_type="young leaves"
/lab hogt="DH10B-T1 phage resistant"
/lone_lb="0R BBa"
/note="Vector:_pAGIBAC1; Site_1: HindIII; Site_2: HindIII"
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Eukaryota, Viridiplantae, Streptophyta, Embryophyta, Tracheophyta,
Spermatophyta, Magnoliophyta, Liliopsida, Poales, Poaceae;
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Enthartoideae; Orygeae; Oryga.

S Kim,H., Yu,Y., Stum,D., Yost,D., Rao,K., Luo,M., Jetty,R.,
Kudrna,D., Muller,C., Hatfield,J., Soderlund,C. and Wing,R.
OMAP Project
Unpublished (2004)
Contact: Rod A. Wing
Arizona Genomics Institute
University of Arizona
Forbes Building Room 303, Tucson, AZ 85721-0036, USA
Tel: 520 625 9595
Fax: 520 621 1259
Email: rwing@genome.arizona.edu
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                                                                                                                                                                                                             Length 2024;
                                                                                     /cell_type="lymphoblast"
/clone_lib="PTB Chimpanzee Male BAC Library"
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.larity 55.3%; Pred. No. 70;
Conservative 0; Mismatches 55; Indels
                                                                                                                                                                                                                                                                   40; Indels
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                                                                                                                                                                                                             DB 10;
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FORWARD: TAA TAC GAC TCA CTA TAG GG
BACKWARD: CAC TCA TTA GGC ACC CCA
Insert Length: 161 Std Error: 0.00
Plate: 0118 row: A column: 16
Seg primer: TAA TAC GAC TCA TAG GG
Class: BAC ends.
                                                                                                                                                                                                       Score 35.2; DI
Pred. No. 61,
0; Mismatches
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/db_xref="taxon:4536"
/clone="OR_BBa0118A16"
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/clone="PTB-066P10.F"
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CL751558.1 GI:50698847
                                                                                                                                                                                                       ch 24.6%;
1 Similarity 59.2%;
58; Conservative
                                                     /sex="male"
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Matches 68; Conserv
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                                  end
of
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Pan troglodytes DNA, clone: PTB-066P10.F, genomic survey sequence.
AG074763
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Mammalia, Butheria, Buarchontoglires, Primates, Catarrhini;
   Tel:81-45-503-9111, Fax:81-45-503-9170)
Clones are derived from the chimpanzee BAC library PTB This BAC
was generated during the R&D process and may have higher chance
clone tracking errors.
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Totoki,Y., Watanabe,H. and Sakaki,Y.
BAC end sequences of Library PTB
Unpublished
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Direct Submission
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Length 1123;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /sex="male"
/cell_type="lymphoblast"
/clone_lib="PTB Chimpanzee Male BAC Library"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                94 GCTCTGCCGGCCCCACCGAGCGAGCGAGCGCGCAGAGAGGGAGTG 138
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1 Similarity 57.1%; Pred. No. 55;
60; Conservative 0; Mismatches 45;
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/organism="Pan troglodytes"
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Pan troglodytes
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R.Site 1 : SacI
R.Site 2 : SacI.
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                                                                                                                                                        Sequencing: M13Rev
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- Web: www.genoscope.cns.fr)

- Web: www.genoscope.cns.fr)

Determination of this BAC-end sequence was carried out as part of collaboration with the Berkeley Drosophila Genome Project (BDGP). The BDGP is constructing a physical map of the Drosophila melanogaster genome using these BACs. For further information please see http://www.fruitfly.org The BDGP Drosophila melanogaster BAC library was prepared by Kazutoyo Googgawa and Aaron Mammoser in Pieter de Jong's laboratory in the Department of Cancer Genetics at the Roswell Park Cancer Institute in Buffalo, NY. The library is named RPCG-98 and was constructed by partial BCORI diseation of Drosophila DNA provided by the BDGP from the isogenic strain v2; cn bw sp, the same strain used for the BDGP's pl and by to order individual BAC clones, the entire library, or filters for hybridization from the BACPAC Resource Center can be found at http://Dacpac.med.buffalo.edu/drosophila_bac.htm.
                                                                                                                                                                                                                                                                       CNSO052P

CNSO052P

Droadphila melanogaster genome survey sequence TET3 end of BAC #
BACRIPIO of RPCI-98 library from Droadphila melanogaster (fruit
fly), genomic survey sequence.

AL056652.1 GI:4932342
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Submitted (02-JUN-1999) Genoscope - Centre National de Sequencage :
BP 191 91006 EVRY cedex - FRANCE (E-mail : segref@genoscope.cns.fr
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498 CGACGAAAGCGGCCCCCCCCCCCCGCTGGCGGCGGCGGCGCGCCCCAATTACGAGGGG 557
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Bukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
Ephydroidea; Drosophilidae; Drosophila.
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/mol_type="genomic DNA"
/db_xref="kaxon:7227"
/clone="BACR11P16"
/clone="BACR11P16"
/clone lib="RPCI-98"
                                                                                                                                                                                                                                                                                                                                                                                                                                                               Drosophila melanogaster (fruit fly)
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                                                                                      139 GGC 141
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Contact: Henrig S
laboraty 123, dept.Lehrach
laboraty 123, dept.Lehrach
Max-Planck-Institut fuer Molekulare Genetik
Innestr.63-73, D-14195 Berlin, Germany
Tel: +49 30 8413 1612
Fax: +49 30 8413 180
Email: henrig@molgen.mpg.de
The library was characterised by oligonucleotide fingerprinting
(ONFP) to reduce sequencing redundancy. According to the ONFP
procedure, clones that display the same hybridisation matrix with a
battery of 200 Bmer oligonucleotides are grouped into clusters. One
clone per ONFP cluster was selected for sequencing. CDNA clones and
filters are distributed via Deutsches Ressourcenzentrum fuer
men per one per one per oligonucleotide are grouped into clusters.
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         BI774214 466238 MA
CN788278 4122596 B
CK831007 4054395 B
CK831007 4054394 B
EX180847 B04_45-77
BX622561 BX622561
CN066332 M11 Ag2_D
BISH431 fm3_C02.9
BM572584 fx55a08.9
BM572584 fx55a08.9
BM57259 BM52039
BW520329 BM52039
BW520329 BM52039
BW520329 BM52039
BK51810 BW534121
AL720322 AL720322
BE19101 HVSMEh008
CK661380 LP20845.5
CK661380 LP20845.5
CK661380 LP20845.5
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CK661380 LP20845.5
BM608179 170006870
BQ986581 QCFI2804.104
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1 (bases 1 to 264)
Hennig, S., Janitz, M., Herwig, R. and Williams, J.

Generation, annotation, evolutionary analysis and database integration of 14969 cattle EST clusters
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FORMARD: 5' CCCCAGGCTTTACACTTTATGCTTCCGGCTCG 3' (M13RSP) 5'-8eq
BACKWARD: 5' GCTATTACGCCAGCTGGCGAAAGGGGGATGTG 3' (M13FSP) 3'-8eq
                                                                                                                                                                                                                                                                                                                                                                                                                                                   BovGen 20573 normal cattle brain Bos taurus cDNA clone RZPDp1056M03600 5', mRNA sequence. CO892248 CO892248:1 GI:51822548
                                                                                                                                                                                                                                                                                                                                                                                                                                       linear
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Location/Qualifiers
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/dev_stage="adult brain"
                                                                                                                                                                                                                                                                                                                                                                   ALIGNMENTS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /mol_type="mRNA"
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/clone="RZPDp1056M03600"
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                                       CK831007
CK982139
CK180847
BX622561
CK068332
BI881431
BM572584
BH589499
BM859438
                                                                                                                                                                                     BW534121
AL720322
BE195101
CR661380
CA296025
BC044003
BM605179
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BW335572 BW335572
AL193990 Tetracdon
CK159167 FGAS04056
CK569196 EST067 Su
AV964990 AV964990
CC046399 MZCCCS2003
CC046199 Lr FRSCO03
CC048199 Lr FRSCO03
CO44819 La Ea44912
BU31297 Gad44912
BU311297 BJ371297
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CO888893 BovGen_17
BH115587 RPCI-24-3
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fk02d02.y
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faa31b10.
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14735.325 Million cell updates/sec
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                                                                                                   November 28, 2005, 18:24:29 ; Search time 5092.96 Seconds
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               GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.
                                                                                                                                                                                                                                                                 41078325 segs, 23393541228 residues
                                                                                                                                                                                                                                                                                              hits satisfying chosen parameters:
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Maximum Match 100%
Listing first 45 summaries
                                                                         - nucleic search, using sw model
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9b_est2::*
9b_est4::*
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9b_est5::*
9b_gss2::*
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Match Length
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Maximum DB E
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/db_xref="taxon:9913"
/clone="RZPDp1056009600"
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Laboraty 123, dept.Lehrach
Max-Planck-Institut fuer Molekulare Genetik
Max-Planck-Institut fuer Molekulare Genetik
Tel: +49 30 8413 1612
Fax: +49 30 8413 1612
Fax: +49 30 8413 1810
Email: hennig@molgen.mpg.de
Email: hennig@molgen.mpg.de
CONFP) to reduce sequencing redundancy. According to the ONFP
procedure, clones that display the same hybridisation matrix with a parcedure, clones that display the same hybridisation matrix with a battery of 200 8mer oligonucleotides are grouped into clusters. One clone per ONFP cluster was selected for sequencing. cDNA clones and filters are distributed via Deutsches Ressourcenzentrum fuer
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                                                                                                                                                                                                                                                                          1241 GTCCCATTTGGGCCAAAATTCCTCACAGATGGACACTTTCACCCGTCTCCTCTTATGG 1300
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/clone_lib="normal cattle brain"
/note="Organ: brain; Vector: pSport1; Site_1: Not1;
Site_2: Sal1, Random primed and directionally cloned in
pSport1 vector using Not1
(5'-pGACTAGTTCTAGATCGCGAGCGCCCC (T)15-3' and Sal1 5'-
TCGACCCACGCGTCCG-3' adapters (Gibco BRL)"
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BACKWARD: 5' GCTATTACGCCAGCTGGCGAAAGGGGATGTG 3' (M13PSP) 3'-8eq
Seq primer: 5'-CCGGTCCGGAATTCCCGGGT-3' (M13RSP).
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                                                                                                                                                                                                                                ;
0
                                                                                                                                                                                  Length 264;
                                                                                                                                                                                Query Match
11.3%; Score 180.8; DB 7; Length
Best Local Similarity 80.3%; Pred. No. 5.2e-42;
Matches 212; Conservative 0; Mismatches 52; Indels
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/mol_type="mRNA"
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Mus musculus (house mouse)

Mus musculus

Mus musculus

Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Bukaryota; Metazoa; Chordata; Glires; Rodentia;

Schurognathi; Murodea; Murinae; Mus.

Schurognathi; Musculae; Murinae; Mus.

Schurognathi; Musculae; Murinae; Mus.

Schurognathi; Musculae; Muslae; Muslaes; Rodentia;

Schurognathi; Musculae; Muslae; Muslaes; Muslaes in Corsolae; Muslaes in Corsolae; Muslaes in Corsolae; Muslaes; 
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Clones are derived from the mouse BAC library RPCI-24. For BAC
Clones are derived from the mouse BAC library availability, please contact Pieter de Jone BACPAC
[pdejong@mail.cho.org). Clones may be purchased from BACPAC
Resources (http://www.chori.org/bacpac/orderingframe.htm). BAC end
page: http://www.tigr.org/tdb/bac_ends/mouse/bac_end_intro.html
Bate: 358 row: F column: 16
Seg primer: T7
Class: BAC ends.
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                         /tissue_type="brain tissue"
/dev stage="adult brain"
/dlone_lib="normal cattle brain"
/clone_lib="normal cattle brain"
/site_2: Sall; Random primed and directionally cloned in
psportl vector using Not!
(5.-pdAcTAGTTGTAGATCGCGAGCGGCCCC (T)15-3' and Sall 5'-
TCGACCCCACGCGTCCG-3' adapters (Gibco BRL)"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1471 AAGCGCTGGAATCCCGAAGTGCAGTACACATCCAATTATGCAAAATCTGCCAACGTTGAT
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/mol_type="genomic DNA"
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/sex="female
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BW335572 Yutaka Satou unpublished cDNA library, adult digestive gland Ciona intestinalis cDNA clone cidg851f15 5', mRNA sequence. BW335572
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                                                                                                                                                                   349
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1 (bases 1 to 581)
Satou,Y., Shin-i,T., Kohara,Y. and Satoh,N.
Expressed genes in Ciona intestinalis (2004)
Unpublished (2004)
Contact: Yutaka Satou
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /organism="Ciona intestinalis"
/mol type="mRNA"
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/tissue_type="digestive gland"
/clone_type="digestive gland"
/clone_lib="tytutaka Satou unpublished cDNA library, adult digestive gland"
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                                     268 acarcaactracereraadecaacaacacatraactracarcaactracarcaactracarca 209
                                                                               230 CCTGGGGGTATTTTGATTTCAACAGATTCCACTGCCACTTTTCACCACGTGACTGGCAGC
                                                                                                                         290 GACTCATCAACAACTTGGGGATTCCGGCCCAAGAGACTCAACTTCAAACTCTTCAACA
                                                                                                                                                                                                           148 rearcaacaacaacaacregrrearcaacaacaacaacregrrearcaacaacaacaacarcarca
170 AAATCTCCAGTGCTTCAACGGGGCCCAGCAACGACAACCACTACTTCGGCTACAGCACCC
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Pred. No. 0.055;
0; Mismatches 190; Indels
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Location/Qualifiers
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Sakyo-ku, Kyoto, Kyoto 606-8502, Japan
Tel: 81-753-4095
Fax: 81-75-705-1113
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Best Local Similarity 45.9%;
Matches 161; Conservative
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Ciona intestinalis
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                                                                           /cell_type="Spleen/Brain"
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/note="Vector: pTARBAC1; Site_1: BamH1; Site_2: BamH1;
// RPCI-24 Mouse BAC Library produced by Pieter de Jong. The library was cloned in the pTARBAC1 cloning vector at the BamH1 sites using MboI partially digested male C57BL/6JDNA."
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                                                                                                                                                                                                                                                                                                                                                                                                                                                     61 AATGCCTCAGGAAATTGGCATTGCGATTCCACATGGCTGGGCGACAGAGTCATCACCACC 120
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1 (bases 1 to 367)
Urushihara,H., Tanaka,Y., Kohara,Y. and Shin-i,T.
Full length cDNA of Dictyostellum discoideum at the vegetative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /dev_stage="Growth phase"
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                                                                                                                                                                                                                                                                                                                                                                 1 ATGGCTTCAGGCGGTGGCGCACCAATGGCAGACAATAACGAAGGCGCCGACGGAGTGGGT
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                                                                                                                                                                                                                                                                         Score 66.8; DB 9; Length 753;
Pred. No. 7.6e-08;
0; Mismatches 62; Indels
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49.6%; Pred. No. 0.023;
tive 0; Mismatches 122; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /organism="Dictyostelium discoideum"
/mol_type="mRNA"
/strain="AX4"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Contact: Tadasu Shin-i
Center For Genetic Resource Information
National Institute of Genetics
1111 Yata, Mishima, Shizuoka 411-8540, Japan
Fax: 81-559-81-6855
                        /db_xref="taxon:10090"
/clone="RPCI-24-358F16"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /db_xref="taxon:44689"
/clone="ddv18d02"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Email: tshini@genes.nig.ac.jp
Location/Qualifiers
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Dictyostelium discoideum
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Best Local Similarity 64.6%;
Matches 115; Conservative (
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                                                                  /sex="Male"
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Matches 120;
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/mol_type="mRNA"
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/cultivar="wheat line PI 178383"
/db xref="texton:4558"
/lab host="PHS alpha"
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/clone_lib="triticum aestivum FGAS: Talt5"
/clone="forgan: Crown; Vector: pGEM-T; SSH (suppression subtractive hybridization) cDNA library from genotype PI178383 cold hardened at 2 C for 21 days and 49 days (equal amount of cDNA pooled together before subtraction, tester) and subtracted against genotype Norstar cold hardened at 2 C for 1 days (24 H) (driver). Modified Smart cDNA (Clontech)priming and non-directional cloning"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Email: fgas estages.usask.ca
This sequence is the direct result of the Base calling software
Phred (default parameters). It is the raw base calls. To aid in the
identification of the high quality insert the software Lucy
(default parameters) has been run on this sequence. Lucy identified
the region [128,636].
Plate: Talt537 row: N column: 23.
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Bukaryota, Viridiplantae, Streptophyta, Embryophyta, Tracheophyta, Spermatophyta, Viridiplantae, Streptophyta, Embryophyta, Tracheophyta, Booideae; Triticae, Triticum.

I (bases I to 89)

Allard,F., Crosby, M.L., Danyluk, J., Eudes,F., Frick, M., Gaudet, D., Genswein,B., Graf,R., Gulick,P., Hrycan,L.D., Laroche,A., Links, M.G., McCarthy,E.L., Monroy,A., Muzak,I., Nilson,D., Pennket,C., Roach, J.L. and Sarhan,F.

Functional Genomics of Abiotic Stress In Wheat and Canola Crops
       271 TCACCACGTGACTGGCAGCGACTCATCAACAATTGGGGATTCCGGCCCAAGAGACTC 330
                                                                                   211 TACTTCGGCTACAGCACCCCCTGGGGGTATTTTGATTTCAACAGATTCCACTGCCACTTT 270
                                                                                                                                                                                                                                                                                                                                                                                                                                                              CK159167 1605-DEC-2
FGASO40564 Triticum aestivum FGAS: Talt5 Triticum aestivum cDNA,
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Best Local Similarity 48.1%; Pred. No. 0.17;
Matches 129; Conservative 0; Mismatches 139;
                                                                                                                                                                                                                                                                                    331 AACTICAAACTCTTCAACATCCAAGTCAAGGA 362

    .869
    /organism="Triticum aestivum"

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Contact: Wm L Crosby
Bioinformatics
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CK159167/c
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                                                                                                                                                                                                                                                     CNSO2EOD 681 bp DNA linear GSS 01-SEP-2000 Tetraodon nigroviridis genome survey sequence T7 end of clone 262H14 of library G from Tetraodon nigroviridis, genomic survey
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AL193990.1 G1:7832096
AL193990.1 G1:7832096
AL193990.1 G1:7832096
GSS, genome survey sequence.
Tetrackon nigroviridis
Tetrackon nigroviridis
Tetrackon nigroviridis
Tetrackon nigroviridis
Tetrackon nigroviridis
Actinopterygii, Neopterygii, Teleostel; Euteleostel;
Actinopterygii, Neopterygii, Percomorpha; Tetrackontiformes;
Tetrackontoidea; Tetrackontidae; Tetrackon.
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                                 447
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Roest Crollius, H., Jaillon, O., Dasilva, C., Ozouf-Costaz, C., Fizames, C., Fischer, C., Bouneau, L., Billault, A., Quetier, F., Saurin, W., Bernot, A. and Weissenbach, J. Characterization and repeat analysis of the compact genome of the freshwater pufferfish Tetraodon nigroviridis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Roest Crollius, H., Jaillon, O., Dasilva, C., Bouneau, L., Fisher, C., Bernot, A., Fizames, C., Mincker, P., Brottier, P., Quetier, F., Saurin, W. and Weissenbach, J.
31 GACAATAACGAAGGCGCCGACGGAGTGGGTAATGCCTCAGGAAATTGGCATTGCGATTCC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Estimate of human gene number provided by genome-wide analysis using Tetracdon nigroviridis DNA sequence Nat. Genet. 25 (2), 235-238 (2000)
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                                                                           383 TCACAACCATCGCTAATAACCTTACCAGCACGGTTCAAGTCTTCTCGGACT 433
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/note="Genoscope sequence ID : COAG262DD07LP1
end : T7"
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                                                                                                                          448 ACAACAACAACGCCTAATACAAGAACAACAAAAACACATCACCAACT
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ilarity 43.4%; Pred. No. 0.15;
Conservative 10; Mismatches 178;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /mol_type="genomic_DNA"
/db_xref="taxon:99883"
/clone="262H14"
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CNS02EOD/c
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                                                                                                                                                                                                                                                                                                                                                                                                                    Ciona intestinalis
Bukazyota, Metazoa, Chordata, Urochordata, Ascidiacea, Enterogona,
Phlebobranchia, Cionidae, Ciona.
1 (bases 1 to 414)
Satoh, N., Satou, Y., Kohara, Y. and Shin-i, T.
Expressed genes in Ciona intestinalis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             171 AATCTCCAGTGCTTCAACGGGGGCCAGCAACGACAACCACTACTTCGGCTACAGCACCCC 230
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        260 CAACAACTGTTGCTACAGGCACAACAGCAACACAACTAATTCAACAACAACAACAA 201
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     291 ACTCATCAACAACTTGGGGATTCCGGCCCAAGAGACTCCAACTTCAAACTCTTCAACAT 350
CIGGCAGCGACTCATCAACAATIGGGGATTCCGGCCCAAGAGACTCAACTICAACT 341
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                                                                                                           140 TTGCAGCAGGCACAACAACAACAACAACAACATGATTCAACAACAACAATTGCTACAG 81
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /tissue_type="whole animal"
/dev stage="young adult"
/clone_lib="Nori Satoh unpublished cDNA library, young
adult"
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                                                                            CITCAACATCCAAGTCAAGGAGGTCACGACGAATGATGGCGTCACAACCATCGCTAATAA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Email: satch@ascidian.zool.kyoto-u.ac.jp.
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /organism="Ciona intestinalis"
|mol_type="mkna"
|db_xref="taxon:719"
|clone="ciad17116"
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AV964990.1 GI:19454686
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Best Local Similarity 46.6%;
Matches 139; Conservative (
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Contact: Nori Satch
Department of Zoology
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Kyoto University
Sakyo-ku, Kyoto, Kyo
Tel: 81-75-753-4081
Fax: 81-75-705-1113
                                                                                                                                                                                                                                                                                                                                                                                                     Ciona intestinalis
                                                                                                                                                      412
                                                                                                                                                                                       452 CAGCAACAGCA 462
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AV964990/c
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Contact: Guihua Bai
USDA/ARS and Department of Agronomy Kansas State University Manhattan, KS 65506, USA
Email: Gbai@bear.agron.ksu.edu
Seq primer: M13 Forward
                                                                                                                                                                                                                                                                                                                                                                                 581 bp mRNA linear EST 08-SEP-2004 Clontech (cat. # K1804-1) Triticum aestivum cDNA CF569196
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                                                                            265 CACTTTTCACCACGTGACTGGCAGCGACTCATCAACAACAATTGGGGATTCCGGCCCCAAG 324
                                                                                                                                                                                         AGACTCAACTTCAAACTCTTCAACATCCAAGTCAAGGAGGTCACGACGAATGATGGCGTC 384
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46.6%; Pred. No. 0.16;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /organism="Triticum aestivum"
                                                                                                                                                                                                                                                                  385 ACAACCATCGCTAATAACCTTACCAGCA 412
                                                                                                                                                                                                                                                                                                       545 AACAACAACAACAACAACAACAACA 518
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Location/Qualifiers
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Triticum aestivum
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Matches 145; Conserv
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VERSION KEYWORDS SOURCE ORGANISM

REFERENCE AUTHORS

DEFINITION RESULT 10 CO465395

ACCESSION

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Chaseley,J., Hedley,B.A., Morgan,J.C., Sturzenbaum,S., Kille,P. and
Blaxter,M.
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Lumbricina, Lumbricidae; Lumbricus.
1 (bases 1 to 748)
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CGACAGAGTCATCACCACCAGCACCCGCACCTGGGCCTTGCCCCACCTACAATAACCACCT 161
                                                     The Lumbricus rubellus EST program - Sequences from a Pluorantene
                                                                                                                                                                                                                                                                                                                                                                      CTGGCAGCGACTCATCAACAATTGGGGATTCCGGCCCAAGAGACTCAACTTCAAACT
                                                                                                                        CTACAAGCAAATCTCCAGTGCTTCAACGGGGCCAGCAACGACAACCACTACTTCGGCTA
                                                                                                                                                                                                                                              CAGCACCCCTGGGGGTATTTTGATTTCAACAGATTCCACTGCCACTTTTCACCACGTGA
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Clone lib="Barthworm Fluorantene Exposure Library"
/note="Westor: pBluescript II SK+; The library was
prepared using protocols given by the supplier
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CO048199

Lr_PAHCF_66A08_SKplus Earthworm Fluorantene Exposure Library
Lumbricus rubellus cDNA clone Lr_PAHCF_66A08, mRNA sequence.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Main College, Museum Avenue, Cardiff, CF11 3TL, Tel: +44 2920876680
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/organism="Lumbricus rubellus"
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Lumbricus rubellus
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/db_xref="taxon:35632"
/clone="Lr_PAHCF_66A08"
/tissue_type="Whole worm"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PCR PRIMERS
FORWARD: gtttcccagtcacgacg
BACKWARD: caggaaacagctatgaccatg
Plate: 66 row: A column: 08
Seq primer: Skplus
High quality sequence start: 8
High quality sequence stop: 524.
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Cardiff University
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CO048199
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//look blost="s. coil blost="s. co
                                                            EST 08-JUN-2005
                                                                                                                                                                                                                                                                                                Eukaryota, Viridiplantae, Streptophyta, Embryophyta; Tracheophyta, Spermatophyta, Magnoliophyta, Liliopsida, Poales; Poaceae, PACCAD clade, Panicoideae, Andropogoneae; Zea.

1 (bases 1 to 801)
Verza, N.C., Silva, T.R., Cord-Neto, G., Nogueira, F.T.S., Fisch, P.H., De Rosa, V.E. Jr., Martins, M.M., Vettore, A.L., da Silva, F.R. and
                                                     CO465395 801 bp mRNA linear EST 08-JUN-20
MZCCS20039C06.g Maize Endosperm cDNA Library Zea mays cDNA, mRNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Endosperm-preferred expression of maize genes as revealed by transcriptome-wide analysis of expressed sequence tags plant Mol. Biol. (2005) In press Contact: Arruda P. Centro de Biologia Molecular e Engenharia Genetica Universidade Estadual de Campinas Caixa Postal 6010, 13083-970, Campinas SP, Brazil Pel: 55 19 3788 1089
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match 2.7%; Score 43.4; DB 7; Length 801; Best Local Similarity 46.3%; Pred. No. 0.73; Matches 143; Conservative 0; Mismatches 166; Indels (
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /organism="Zea mays"
/mol_type="mRNA"
/culfivar="f=:35 near isogenic line"
/db xref="taxon:457"
/sex="hermaphrodite"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              'tissue_type="endosperm"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Email: parruda@unicamp.br.
Location/Qualifiers
                                                                                                                                                                                 GI:67039140
                                                                                                                                                                              CO465395.1
                                                                                                                  sequence.
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Zea mays
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FEATURES

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Length 748;

2.7%; Score 43.2; DB 51.6%; Pred. No. 0.82;

Query Match Best Local Similarity

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                                                                                                                            111 CATCACCACCAGCACCCGGACCTGGGCCTTGCCCACCTACAATAACCACCTCTACAAGCA 170
                                                                                                                                                                       171 AATCTCCAGTGCTTCAACGGGGCCAGCAACGACAACCACTACTTCGGCTACAGCACCCC 230
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      plant genomics programme 'Genoplante' (http://www.genoplante.com and http://genoplante-info.infoblogen.fr).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           93, rue Henri Rochefort 91025 EVRY CEDEX France
Tel: 33 1 69 47 54 00
Fax: 33 1 69 47 54 10
This sequence has been generated in the framework of the french
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/clone="6608118C06"
/tissue_type="grain (608 degrees per day after
/clone_lib="G608"
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                                        Length 415;
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                                                                                                                                                                                                                                                                                                                     231 CTGGGGGTATTTTGATTTCAACAGATTCCACTGCCACT 268
                                                                               72;
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                                        DB 2;
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                                                                0.86;
                                        Score 42.8; D
Pred. No. 0.86
0; Mismatches
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/cultivar="recital"
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                                        2.7%;
1 Similarity 54.4%;
86; Conservative
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Matches 86; Conserv
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/clone_lib="zebrafish Research Genetics C32 fin"
/note="vector: py773D-pac with a modified polylinker;
Site_l: EcoR1; Site_2: Not1; lst strand cDNA was prepared
from_zebrafish(C32) fin, and was then primed with a Not I
- oligo(dT) primer. Double-stranded cDNA was ligated to
Eco R adaptors (Pharmacia), digested with Not I and
cloned into the Not I and Eco RI sites of the modified
pT7T3 vector. Library is non-normalized. Library was
constructed by Ning Wu. NOTE: This clone is available
royalty-free through LiAL, contact the IMAGE Consortium
(info.llnl.gov)for further information"
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fk95c07.yl Zebrafish Research Genetics C32 fin Danio rerio CDNA 5'
similar to contains element TAR1 repetitive element ;, mRNA
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(bases 1 to 415)

Clark,M., Johnson,S.L., Lehrach,H., Lee,R., Li,F., Marra,M., Eddy,S., Hillier,L., Kucaba,T., Martin,J., Beck,C., Wylie-T., Underwood,K., Steptoe,M., Theising,B., Allen,M., Bowers,Y., Person,B., Swaller,T., Gibbons,M., Pape,D., Harvey,N., Schurk,R., Ritter,E., Kohn,S., Shin,T., Jackson,Y., Cardenas,M., McCann,R., WashU Zebrafish Est Project 1998
Unpublished (1998)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Genome
                                             114 CACCACCAGCACCCGCACCTGGGCCTTGCCCACTACAATAACCACCTCTACAAGCAAAT 173
                                                                                      79 cgcccachachaccacracracracracrccaccrccracraccaccacaca 138
                                                                                                                                                                                 199 ceacriaceaceceaciaiciaaceacriceacriceacereceacereceaceaceae 258
                                                                                                                                                                                                                              234 GGGGTATTTTGATTTCAACAGATTCCACTGCCACTTTTCACCACGTGACTGGCAGCGACT 293
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                                                                                                                                      174 CTCCAGTGCTTCAACGGGGCCAGCAACGACAACCACTACTTCGGCTACAGCACCCCCTG
  Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Contact: Srephen L. Johnson
Washington University School of Medicine
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108, USA
TTE1: 314 286 1800
Fax: 314 286 1810
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Email: zbrafish@watson.wustl.edu
cDNA Library Preparation: Ning Wu. cDNA Library Arrayed by:
Research Genetics. DNA Sequencing by: Washington University
Sequencing Center Clone distribution: Research Genetics web
address: http://www.researchgenetics.com/
Seq primer: T3 ET from Amersham
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93,
    Mismatches
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/mol_type="mRNA"
/db_xref="taxon:7955"
/tissue_type="Fin"
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BJ371297 linear EST 08-MAR-2002 BJ371297 Dictyostelium discoideum cDNA library, CF Dictyostelium discoideum cDNA clone ddc57m07 5', mRNA sequence.
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Dictyostelium discoideum
Dictyostelium discoideum
Eukaryota; Mycetozoa; Dictyosteliida; Dictyostelium.
1 (bases 1 to 450)
Urushihara,H., Tanaka,Y., Kohara,Y. and Shin-i,T.
Full length cDNA of Dictyostelium discoideum at the culmination
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /dev_stage="Culmination stage"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                102 GGACAGAGTCATCACCACCAGCACCCGCACCTGGGCCTTGCCCACCTACAATAACCACCT
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2.6%; Score 42.2; DB 3; Length 45
Best Local Similarity 46.0%; Pred. No. 1.3;
Matches 143; Conservative 0; Mismatches 168; Indels
                            CAGCACCCCCTGGGGGTATTTTGATTTCAACAGATTCCACTGCCACT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /organism="Dictyostelium discoldeum"
/mol_type="mRNA"
/strain="AX4"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Contact: Tadasu Shin-i
Center For Genetic Resource Information
National Institute of Genetics
1111 Yata, Mishima, Shizuoka 411-8540, Japan
Fax: 81-559-81-6855
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Search completed: November 29, 2005, 14:17:59
Job time : 5096.96 secs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /db_xref="taxon:44689"
/clone="ddc57m07"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Email: tshini@genes.nig.ac.jp.
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                               BJ371297.1 GI:19280680
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/lab_hogt="Vector pBk-CMV; Site 1: Ecoti; Site 2: XhoI; lst
strand cDNA primed with (GA)IDACTAGTCTCGAG(T)18, followed
by second strand synthesis, and ligated to 5' adapter
(5')-aattcggcacgag- 3', 3'-gccgtgctc-5'. cDNA was cloned
directionally (Ecoti, XhoI) into Stratagene Zap express
landca phage arms. Mass invivo excision done to obtain
inserts in pBK-CMV phagemid."
                                                                                                                                                                                                                                                                                                                                                                                                      Eukaryota; Metazoa; Chordata, Craniata; Vertebrata; Euteleostomi; Actinopterygii; Neopterygii; Teleostei; Ostariophysi; Cyprinidae; Danio.

Cypriniformes; Cyprinidae; Danio.

I (bases 1 to 435)

Clark,M., Johnson,S.L., Lehrach,H., Lee,R., Li,F., Marra,M., Eddy,S., Hiller,L., Kucaba,T., Martin,J., Beck,C., Wylie,T., Person,B., Sweller,T., Glabons,M., Pape,D., Harvey,N., Schurk,R., Ritter,E., Kohn,S., Shin,T., Jackson,Y., Cardenas,M., McCann,R., Waterston,R. and Wilson,R.

Unpublished (1998)

Contect: Stephen L. Johnson
                                                                                                                             faa44g12.y1 zebrafish fin day3 regeneration Danio rerio CDNA clone IMAGE:5912254 5' similar to contains element MER1 repetitive element 1, mRNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Washington University School of Medicine
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108, USA
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108, USA
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108, USA
141 286 1810
Email: zbrafish@watson.wustl.edu
Email: zbrafish@watson.wustl.edu
Email: zbrafish@watson.wustl.edu
Mathew Clark. DNA Sequencing by: Washington University Genome
Sequencing Cencer Clone distribution: Genome Systems, St. Louis,
Missouri (web address: www.genomesystems.com) (email contact:
Info@genomesystems.com) and Research Genetics, Huntsville, Alabama
(web address: www.resgen.com) (email contact: info@resgen.com) and
RessourcenZentrumPrimarDatenbank, Berlin, Germany (web address:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        181 CAACTGCGGCTTCAGCAACTACACCTACAACTGCGGCTTCAGCAACTACACCCCACAACTG 240
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2.6%; Score 42.2; DB 5; Length 435;
Best Local Similarity 53.3%; Pred. No. 1.3;
Matches 89; Conservative 0; Mismatches 78; Indels (
/organism="Danio rerio"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        www.rzpd.de)
Seq primer: T3 ET from Amersham
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Location/Qualifiers
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BQ449242.1 GI:21252354
                                                                                                                                                                                                                                                                                                                                                         Danio rerio (zebrafish)
                                                                                                                                                                                                                                                                                                                                                                                        Danio rerio
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VERSION
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SOURCE
ORGANISM
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DEFINITION
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JOURNAL
COMMENT
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Gaps

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221

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Sequence 16, Application US/09807802A

TITLE OF INVENTION: Adeno-Associated Virus Serotype I Nucleic Acid Sequences,

TITLE OF INVENTION: Vectors and Host Cells Containing Same

TITLE OF INVENTION: Vectors and Host Cells Containing Same

FILE REFERENCE: GNVPN.031USA

CURRENT APPLICATION NUMBER: US/09/807,802A

CURRENT FILING DATE: 1998-11-05

PRIOR PLILNG DATE: 1998-11-05

PRIOR PLILNG DATE: 1999-11-02

NUMBER OF SEQ ID NOS: 20

SOFTWARE: PatentIn version 3.1

SEQ ID NO 16

LENGTH: 1605
                                                     Sequence 9, Appli
Sequence 7, Appli
Sequence 1, Appli
Sequence 2, Appli
Sequence 1, Appli
Sequence 1, Appli
Sequence 4, Appli
Sequence 4, Appli
Sequence 2, Appli
Sequence 3, Appli
Sequence 3, Appli
Sequence 1261, Ap
Sequence 1261, Ap
Sequence 1261, Ap
Sequence 165983,
Sequence 165983,
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100.0%; Score 1604; DB 3; Length 1605;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1604; Conservative 0; Mismatches 0; Indels 0;
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US-09-533-427-9

US-09-533-427-1

US-08-533-427-1

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US-08-588-955A-1

US-08-928-361B-1

US-08-928-361B-1

US-08-928-361B-4

US-08-928-361B-4

US-08-928-361B-4

US-08-928-361B-3

US-08-928-361B-3

US-09-988-995A-4

US-08-928-361B-3

US-09-988-95A-3

US-09-988-95A-3

US-09-988-95A-3

US-09-902-540-1261

US-09-949-016-16593

US-09-949-016-16593

US-09-949-016-16593

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US-09-949-016-16593
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     LOCATION: (1)...(1602); OTHER INFORMATION:
US-09-807-802A-16
     ORGANISM: AAV-1
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                                                                                                                                                                                                          November 28, 2005, 19:15:02; Search time 228.137 Seconds (without alignments) 12497.813 Million cell updates/sec
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Sequence 1
Sequence 3
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/cgn2_6/ptcdata/1/ina/5_COMB.seq:*
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/cgn2_6/ptcdata/1/ina/RE_COMB.seq:*
                                         GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.
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US-09-807-802A-14
US-09-807-802A-12
US-09-807-802A-1
US-10-20-807-802A-1
US-09-807-802A-1
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US-09-782-378A-1
US-09-438-268-1
US-09-438-268-1
US-09-438-268-1
US-09-532-5948-17
US-09-532-5948-17
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1604
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Maximum Match 100%
Listing first 45 summaries
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Maximum DB seq length: 2000000000
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Oy 1321 CCGCCTCCTCAGATCCTCAAAACACGCCTGTTCCTGCGAATCCTCCGGCGGAGTTT 1380 1321 CCGCCTCCTCGGATCCTCATCAAAACACGCCTGTTCCTGCGAATCCTCCGGCGGAGTTT 1380 Oy 1381 TCAGCTACAAAGTTTGCTTCATTCATCCCCAATACTCCACAGGACAAGTGAGTG	pplication US/09807802A 2337 VION: Hear, James M. Hear, Weidend-Associated Virus Serotype I Nucle TION: Adeno-Associated Virus Serotype I Nucle TION: Vectors and Host Cells Containing Same S: GNVPN: 031028 TION NUMBER: US/09/807,802A TION NUMBER: US 60/107,114 ATE: 1998-11-05 IION NUMBER: PCT/US99/25694 ATE: 1999-11-02 IID NOS: 20 III NOS: 20 ATE: 1999-11-03 III NOS: 20 ATE: 1999-11-03 ATE: 1990-11-03	Query Match
241 TITGATITCAACAGATICCACTGCCACTITICACCACGTGACTGGCAGCGACTCATCAAC 300 241 TITGATITCAACAGATICCACTGCCACTTITCACCACGTGACTGGCAGCGACTCATCAAC 300 301 AACAATIGGGGATICCGGCCCAAGAGACTCAACTTCAACATCTACAAGTCAAG 360 301 AACAATIGGGGATICCGGCCCAAGAGACTCAACTTCAACATCCAACATCAAG 360 301 AACAATIGGGGATICCGGCCCAAGAGACTCAACTTCAACATCCAAGTCAAG 360 301 GAGGTCACGACGATGATGGCGCCAAGAGACTCAACTTCAACATCCAAGTCAAG 360 361 GAGGTCACGACTACGAGACATCACATCGCTAACAGCACCAGGGTTCAA 420 421 GTCTTCTCGGAATTACGGTACCATCGCTAATAACCTTACCAGGACTCAA 420 421 GTCTTCTCGGAATTACCGAATACGTTCCGGACCAGGGCTGC 480 481 CTCCTCCTCGGAATTACCGGAATACGGCTACCTACCAGGGCTCAAC 540 481 CTCCCTCCGTTCCCGGAACTACTATATACCGCTACCTACC	CTCAG CTCAG CTCAG CTCAC	961 GCTATGGCCTCACAAAACGACGAAGACTCTTTCCCATGAGCGTGTCATGATT 1020 961 GCTATGGCCTCACAAAAGCGACGAAGACTCTTCCCATGAGCGGTGTCATGATT 1020 1021 TTTGGAAAAGAGCGCCGAGCGAAGACTCTTTCCCATGAGCGGTGTCATGATT 1020 1021 TTTGGAAAAGAGGCGCCGGAGCTTCAAACACTGCATTGGACAATGTCATGATTACAGAC 1080 1081 GAAGAGGAAATTAAAGCCCTGAGCCTCGCATGCATTGGACAATGTCATGATTACAGAC 1080 1081 GAAGAGGAAATTAAAGCCACTAACCCTGTGGCCACCGAAAGATTTGGGACCGTGGCAGTC 1140 1141 AATTTCCAGAGCACAGACACAGACCTGCGCACCAGAAGATTTGGGACCGTGGCATTA 1200 1141 AATTTCCAGAGCACAGACACAGACCTGCGCACCAGAAGATTTGGGACCGTGGCATTA 1200 1141 AATTTCCAGAGCACAGACACAGACCTGCGACCAGAAGATTTGGGACCATATGGGCATTA 1200 1141 AATTTCCAGAGCACAGACCTGCGACCCGCAAGATTATGGGCCAAAATT 1260 1201 CCTGGCATGGTGGCAAGATAGAGACCTGCAGGACCCATTTGGGCCAAAATT 1260 1201 CCTGGCATGGTGGCAAGATAGAGACCTGCAGGGTCCCATTTGGGCCAAAATT 1260 1261 CCTCGACAAGATGGAAGATTCACCCTGCTATGGGGGCCTATTGGGCCAAAATT 1260 1261 CCTCGACAAGATGGAACTTCACCCTGCTATGGGGCGCCATTGGGCCAAAATT 1260 1261 CCTCGACAAGATGGAACCTTCACCCTCTTATGGGCCCATTTGGGCCAAAATT 1260 1261 CCTCGACAAGATGGACACTTTCACCCGTCTCCTCTTATGGGCCCAAAATT 1260 1261 CCTCGACAAGATGGACACTTTCACCCGTCTCCTCTTATGGGCCCATTGGACTCAAAATT 1260 1261 CCTCACACAAATGGACCCTCTCTTATGGGCGGCTTTTGGACTCCAAAATT 1260 1261 CCTCACACAAATGGACCCTTCTCTCTCTTATGGGCCCATTGGACTCCAAAATT 1200 1261 CCTCACACAAATGGACCCTTCTCTCTTATGGGCGCCTTTTGGACTCCAAAATT 1200 1261 CCTCACACAAATGGACCCTTCTCTCTTATGGGCGGCTTTTGGACTCCAAAATT 1200 1261 CCTCACACAAATGGACCCTCTCTTATGGGCGGCTTTTGGACTCCAAAATT 1200 1261 CCTCACACAAATGGACCCTCTCTTATGGGCGGCTTTTGGACTCCAAAATT 1200 1261 CCTCACACAAATGGACCCTCTCTTATGGGCGGCTTTTGGACTCCAAAATT 1200 1261 CCTCACACAAATGGACCCTTCTCTCTTATGGGCGGCTTTTGGACTCCAAAATT 1200 1261 CCTCACACAAATTCACCCGTCTCCTCTTATGGGCGGCTTTTGGACTCCAAAATT 1200 1261 CCTCACACAAATTCACCCGTCTCTCTTATTGGGCGCCAAAATT 1200 1270 CCTGCAAAATTACACCCTTTATGGGCGGCTTTTGGACTCCAAAATT 1200 1271 CCTGCAAAATTACACCCTTTATGGGCGCCAAAATT 1200 1271 CCTGCAAAATTACACCCTTTATGGGCGCCTTTTGGGCAAAATT 1200 1271 CCTGCAAAATTACACCTTTATGACTTATGACTCTATTATGACTTATATATTATATATA

	RESULT 3 US-09-807-802A-12 IS-09-807-802A-12 Sequence 12, Application US/09807802A Fatent No. 6759237 GENERAL INFORMATION: APPLICANT: Wilson, James M. APPLICANT: Wilson, James M. APPLICANT: Mison, James M. APPLICANT: Wilson, James M. TITLE OF INVENTION: Vectors and Host Cells Containing Same TITLE OF INVENTION: Vectors and Host Cells Containing Same FILE REFERENCE: GNVPN.031USA CURRENT APPLICATION NUMBER: US/09/807,802A CURRENT FILING DATE: 1999-11-05 FRIOR PTLING DATE: 1999-11-05 FRIOR FILING DATE: 1999-11-02 SOFTWARE: PatentIn Version 3.1 SEQ ID NO 12 LENGTH: 2211 FRATURE: CORGANISM: AAV-1 FRATURE: NAME/KEY: CDS NAME/KEY:	Ouery Match Best Local Similarity 100.0%; Score 1604; DB 3; Length 2211; Best Local Similarity 100.0%; Pred. No. 0; Matches 1604; Conservative 0; Mismatches 0; Indels 0; Gaps 0; Matches 1604; Conservative 0; Mismatches 0; Indels 0; Gaps 0; ArGGCTTCAGGCGTGGCGCAATGGCAATAACGAAGGCGCCGACGGATGGT 60
301 AACAATTGGGGGTTTCCGGCCCAAGAGACTCAACTTCAACTCTTCAACATCCAAGTCAAG 360 496 AACAATTGGGGATTCCGGCCCAAGAGACTCAACTTCAACATCCAACTCCAAGTCAAG 350 496 AACAATTGGGGATTCCGGCCCAAGAGACTCAACTTCAACATCCAAGTCAAG 555 361 GAGGTCACGACGAATGATGGCGTCACAACATCGCTAATAACCTTACCAGCACGGTCAA 420 556 GAGGTCACGAATGATGGCGTCACAACCATCGCTAATAACCTTACCAGCACGGTTCAA 615 421 GTCTTCTCGGAATGATGGCGTCACAACCATCGGTCTCGGCTCTGGGCTCA 615 616 GTCTTCTCGGAATGATGATGATTCCTAACCATCGGCTCTGGGCTCCAGGGCTGC 675 617 [

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Sequence 1. Application US/09807802A

Patent No. 6759237

GENERAL INFORMATION

APPLICANT: Wilson, James M.

APPLICANT: Xiao, Weidong

TITLE OF INVENTION: Adeno-Associated Virus Serotype I Nucleic Acid Sequences,

TITLE OF INVENTION: Adeno-Associated Virus Serotype I Nucleic Acid Sequences,

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TITLE OF INVENTION: Adeno-Associated Virus Serotype I Nucleic Acid Sequences,

FILE REFERENCE: GNVPN.031USA

CURRENT FILING DATE: 1050-102

PRIOR FILING DATE: 1999-11-05

PRIOR FILING DATE: 1999-11-02

NUMBER OF SEQ ID NOS: 20

SOFTHARE: PatentIn version 3.1

SEQ ID NO 1

LENGTH: 4718
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                                TCCAATTATGCAAAATCTGCCAACGTTGATTTTACTGTGGACAACAATGGACTTTATACT
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iive 0; Mismatches
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Best Local Similarity 100.
Matches 1604; Conservative
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| LOCATION: (2223) .. (4430)
| GTHER INFORMATION:
| US-09-807-802A-1
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LOCATION: (335)..(2206)
OTHER INFORMATION:
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ORGANISM: AAV-1
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GAGGTCACGACGATGATGATGGCGTCACAACCATCGCTAATAAACCTTACCAGCAGCAGCACCATCAA
                                                   GICTICICGAACICGGAGIACCAGCTICCGIACGICCTCGGGCTCTGCGCACCAGGGCTGC
                                                                                                                    CTCCCTCCGTTCCCGGCGGACGTGTTCATGATTCCGCAATACGGCTACCTGACGCTCAAC
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Sequence 11, Application US/10216870

Parent No. 6723551

GENERAL INFORMATION:

APPLICANT: KOTIN, ROBERT M

APPLICANT: URABE, MASARE, MASARE,

APPLICANT: PRODUCTION OF ADENO-ASSOCIATED VIRUS IN INSE

FILE REPERENCE: 402133

CURRENT APPLICATION NUMBER: US/10/216,870

CURRENT FILING DATE: 2002-08-13

NUMBER OF SEQ ID NOS: 24

SOFTWARE: Patentin version 3.1

SEQ ID NO 11

LENGTH: 7447
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Best Local Similarity 100.0%; Pred. No. 0;
Matches 1604; Conservative 0; Mismatches
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Sequence 19, Application US/09807802A

Patent No. 6759237

GENERAL INFORMATION:
APPLICANT: Wilson, James M.
APPLICANT: Wilson, James M.
TITLE OF INVENTION: Adeno-Associated Virus Serctype I Nucleic Acid Sequences,
TITLE OF INVENTION: Vectors and Host Cells Containing Same
TITLE OF INVENTION: Vectors and Host Cells Containing Same
FILE REPERENCE: GAVPON.031USA
CURRENT FILING DATE: 1902-02-21
FRIOR APPLICATION NUMBER: US 60/107,114
PRIOR APPLICATION NUMBER: PCT/US99/25694
FRIOR APPLICATION NUMBER: PCT/US99/25694
FRIOR PILING DATE: 1999-11-02
NUMBER OF SEQ ID NOS: 20

SOFTWARE: Patentin version 3.1
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Best Local Similarity 96.4%;
Matches 1547; Conservative
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TYPE: DNA
ORGANISM: AAV-6
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Pred. No. 0;
0; Mismatches
PRIOR APPLICATION NUMBER: US 60/178,536
PRIOR FILING DATE: 2000-01-26
NUMBER OF SEQ ID NOS: 8
SEQ ID NO 4
LENGTH: 4072
                                                                                                                                      ; OTHER INFORMATION: recombinant DNA US-09-770-315-4
                                                                                                                                                                                 Query Match 64.0%;
Best Local Similarity 77.9%;
Matches 1250; Conservative
                                                                                            TYPE: DNA
ORGANISM: Unknown
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APPLICANT: Chiron Corporation
TITLE OF INVENTION: Recombinant AAV Packaging Systems
FILE REFERENCE: 20263-501
CURRENT APPLICATION NUMBER: US/09/770,315
CURRENT FILING DATE: 2001-01-26
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3-09-770-315-4
Sequence 4, Application US/09770315
Patent No. 6429001
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TITLE OF INVENTION: AAV VECTORS AND METHODS
FILE REFERENCE: 28335/85960/8
CURRENT PELLOR NUMBER: US/10/038,972A
CURRENT FILING DATE: 2002-01-04
PRIOR APPLICATION NUMBER: US 60/260,124
PRIOR FILING DATE: 2001-01-05
NUMBER OF SEQ ID NOS: 18
SOFTWARE: Patentin version 3.1
SEQ ID NO 12
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DB GAAGAGGAAGGCTCAGAGAAAACAAATGTGGACATTGAAAAGGTCATGATTACAGAC 3885 OB GAAGAGGAAATTAAAGCCACTAACCCTGGGCCACCGAAGATTTGGGACCGTGCCAGCC 1140	1321 CGGCTCCTCAGATCTCAGATCTCCCCTCTCCCGAATCTCTCGGGGGGTTT 138 120 CCGCCTCCTCCGGTACTTCTCTCCGGAATCCTCCGGGGGGTTT 138 120 CCGCCTCCTCCAGATCCTTCGCGGGGGTTT 138 120 CCTCCTCCAGATCTCTCATCAGAGACAGCCCCGGAACCTTCGTCGACTCTTCGTCGATCCTTCGTCGACTCGTCGAATCTTCTTCGTCGATGTCGACTCGTCGAATCTTCTTCGTCGATGTCGAATCCTTCGTCGAATCCTTCGTCGAATCCTTCGTCGAATCCTTCGTCGAATCCTGGGGAATCCCTGGGAATCCCGGAAGTCGAGGTCAGCTCGTCGTCGTTCGT	Qy 1501 TCCAATTATGCAAAATCTGCCAACGTTGATTTTACTGTGGACAACAACGACTTTATACT 1560 Db	RESULT 9 US-09-770-315-3 Sequence 3, Application US/09770315 Patent No. 6429001 GENERAL INFORMATION: GENERAL INFORMATION: TITLE OF INVENTION: Recombinant AAV Packaging Systems TITLE OF INVENTION: NUMBER: US/09/770,315 FILE REFERENCE: 2006-01-26 PRIOR PAPLICATION NUMBER: US 60/178,536 PRIOR FILING DATE: 2000-01-26 PRIOR FILING DATE: 2000-01-26 NUMBER OF SEQ ID NOS: 8 SOFTWARE: FastSEQ for Windows Version 3.0 SEQ ID NO 3.6	TYPE: DNA 1

301 AACAATTGGGGATTCCGGCCCAAGAACTCCAACTTCAACTCTTCAACATCCAAGTCAAA 3165 310 AACAATTGGGGATTCCGGCCCAAGAACTCCAACTCTTCAACTCTAAATCCAAA 3165 311 GAAGTCCAGCACCACCACCAACTCCAACTCTTTAACTTCAAGTCCAAA 3165 312 GAAGTCCAGCACCACCAACACTCCAACTCCTAACCTTACCAGCACGGTTCAG 3225 312 GAAGTCCAGCACACACACTCCCAACACTCCAGCACCACTCAGCACTCAGG 3225 312 GAGGTCACGACACACACACCACCACTCCCAAAACCTTACCAGCACGGTTCAG 3225 313 GAGGTCACGACACACACACCACACACACACACACACACAC	961 GCTATGGCCTCACACAAAGACGACGAAGCATTCTTCCCATGAGCGGTCATGATT 1020 3766 GCCATGGCAAGCAAGAACGATGAAGAAAGTTTTTTCCTCAGAGCGGGGTTCTCATC 3766 GCCATGGCAAGCCAAGAAAGTTTTTTCCTCAGAGCGGGGTTCTCATC 3825 1021 TTTGGAAAGAGCGCCGGAGCTTCAACACTGCATTGGACATGATTACAGAC 1080 3826 TTTGGAAAGACAAGAAGAAAAATGTGGACATTGGACATGATTACAGAC 1080 1081 GAAGAGGAAATTAAGCCACTAACACTGTGGCAACATTTGGACCATGATTACAGAC 3885 1081 GAAGAGGAAATTAAGCCACTAACACTGTGGCACCATATTGGACCATGATTACAGAC 3885 1081 GAAGAGGAAATTAAGCCACTAACACACGAGCAGTATGGATTTGGACCATGATTACAGAC 3885 1141 AATTTCCAGAGCAACACAACACAGACCAGAGCATCATGGACATTATTACAGACATTATTAGAGACATTATTAGATTATTACAGACATTATTAGATTATTAGATTATTACAGACATTATTAGATTATTAGATTATTAGATTATTAGATTATTAGATTATT
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                                                                       TCCAATTATGCAAAATCTGCCAACGTTGATTTTACTGTGGACAATGGACTTTATACT
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AGTGCGGCAAAGTTTGCTTCCTTCACACACAGTACTCCACGGGACAGGTCAGCGTGGAG
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63.7%; Score 1021.4; DB 3; Length 8179;
Best Local Similarity 78.1%; Pred. No. 0;
Matches 1255; Conservative 0; Mismatches 346; Indels 6;
                                                                                                                                                                Sequence 5, Application US/09438268

Patent No. 6491907

GENERAL INFORMATION:
APPLICANT: Rabinowitz, Joseph E.
APPLICANT: Samulski, Richard J.
APPLICANT: Samulski, Richard J.
APPLICANT: Samulski, Richard J.
APPLICANT: Stao, Weidong
TITLE OF INVENTION: THE SAME
FILE REPRENCE: 5470-186
CURRENT APPLICATION NUMBER: US/09/438,268
CURRENT FILING DATE: 1999-11-10
EARLIER APPLICATION NUMBER: 60/107,840
EARLIER APPLICATION NUMBER: 60/107,840
EARLIER APPLICATION NUMBER: 60/123,651
EARLIER RELING DATE: 1999-11-10
SERLING DATE: 1999-11-10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ; TYPE: DNA
; ORGANISM: Virus
US-09-438-268-5
                                                                                                                                                                                                                                     RESULT 11
US-09-438-268-5
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                                    AACAATTGGGGATTCCGGCCCAAGAGACTCAACTTCAAACTCTTCAACATCCAAGTCAAG
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ACATCCAATTATGCAAAATCTGCCAACGTTGATTTTACTGTGGACAACAATGGACTTTAT
                                4236 ACTTCCAACTACAACAAGTCTGTTAATCGTGGACTTACCGTGGATACTAATGGCGTGTAT
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                                                                                       4296 TCAGAGCCTCGCCCCATTGGCACCAGATACCTGACTCGTAATCTGTA 4342
                                                                                                                                                                                                                                                 APPLICANT: Johnson, Philip R.
TITLE OF INVENTION: Adeno-Associated Virus Materials and
TITLE OF INVENTION: Methods
NUMBER OF SEQUENCES: 3
CORRESPONDENCE ADDRESS:
ADDRESSEE: Marshall, O'Toole, Gerstein, Murray & Borun
                                                                    1558 ACTGAGCCTCGCCCCATTGGCACCCGTTACCCTTACCCGTCCCCTGTA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                    ZIP: 60606
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IS OF Compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/254,358
FILING DATE:
CLASSIFICATION: 435
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Pred. No. 0;
0; Mismatches 358;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match 62.6%; Score 1004.2; Best Local Similarity 77.4%; Pred. No. 0; Matches 1243; Conservative 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                 Gerstein,
S. Wacker
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ATTORNEY AGENT INFORMATION:
NAME: NO. 558785and, Greta E.
REGISTRATION NUMBER: 35.302
REFERENCE/DOCKET NUMBER: 31975
TELECOMMUNICATION INFORMATION:
TELEPHONE: (312) 474-6300
TELEFAX: (312) 474-6300
TELEFAX: 25-3856
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
SEQUENCE CHARACTERISTICS:
TYPE: nucleic acid
STRANDEDNESS: Single
                                                                                                                                                                                                                                                                                                                                               3: Marshall, O'Toole,
6300 Sears Tower, 233
                                                                                                                                                                                                  Sequence 1, Application US/08254358
Patent No. 5658785
GENERAL INFORMATION:
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MOLECULE TYPE: DNA (genomic)
                                                                                                                                                                                                                                                                                                                                                                STREET: 6300 Sear
CITY: Chicago
STATE: Illinois
COUNTRY: USA
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                                                                                     1440 AATTGAATGGGAGCTGCAGAAAGAAACAGCGCAGGCTGGAATCCCGAAGTGCAGTACAC
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Pred. No. 0;
0; Mismatches 358; Indels
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Methods
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MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/475,391
FILING DATE: 07-JUN-1995
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/254,358
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: NO. 5786211and, Greta E.
REGISTRATION NUMBER: 35,302
REFERENCE/DOCKET NUMBER: 31975
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Murray
Drive
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Gerstein, S. Wacker
                                                                                                                                                                                                                                                                                                                                                                                                                                   NUMBER OF SEQUENCES: 3
CORRESPONDENCE ADDRESS:
STREET: 6300 Sears Tower, 233 S.
CITY: Chicago
STATE: 111inois
COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                 Sequence 1, Application US/08475391
Patent No. 5786211
GENERAL INFORMATION:
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TELEFAX: (312) 474-0448
TELEX: 25-3856
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 4680 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
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Best Local Similarity 77.4%;
Matches 1243; Conservative (
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                                         4006 CCAGGCATGGTCTGGCAGGACAGAGATGTGTACCTTCAGGGGCCCATCTGGGCAAAGATT
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TITLE OF INVENTION: Adeno-Associated Virus Materials of TITLE OF INVENTION: Methods
NUMBER OF SEQUENCES: 3
ADDRESSEE: Marshall, O'Toole, Gerstein, Murray & Bo STRET: 6300 Sears Tower, 233 S. Wacker Drive STRET: Chicago STATE: 1111nois
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              mEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
ODERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PAtentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/709,609
FILING DATE:
CLASSIFICATION: 435
ATTORNEY/ACRAM
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NAME: No. 5858775and, Greta E.
REGISTRATION NUMBER: 35,302
REFERENCE/DOCKET NUMBER: 31975
TELECOMMUNICATION INFORMATION:
TELEPHONE: (312) 474-6300
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 1, Application US/08709609
Patent No. 5858775
GENERAL INFORMATION:
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INFORMATION FOR SEQ ID NO: 1
SEQUENCE CHARACTERISTICS:
LENGTH: 4680 base pairs
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STRANDEDNESS: single
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COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
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Pred. No. 0;
0; Mismatches 358; Indels
                                                                            TOPOLOGY: linear

MOLECULE TYPE: DNA (genomic)

PCT-US95-07178-1
                                                                                                                                                                                       Query Match 62.6%;
Best Local Similarity 77.4%;
Matches 1243; Conservative
LENGTH: 4680 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
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; GENERAL INPORMATION:
APPLICANT: JOHNSON, Philip R.
TITLE OF INVENTION: Methods
TITLE OF INVENTION: Methods
CORRESPONDENCES:
CORRESPONDENCE ADDRESS:
ADDRESSEE: Marshall, O'Toole, Geretein, Murray & Borun STREET: 6300 Sears Tower, 233 S. Wacker Drive CITY: Chicago
STATE: Illinois
COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TGAGCCTCGCCCATTGGCACCCGTTACCTTACCCGTCCCTGTA 1604
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MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
GURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US95/07178
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FILING DATE:
CLASSIPICATION:
ATTORNEY/AGENT INFORMATION:
NAME: Noland, Greta E.
REGISTRATION NUMBER: 35,302
REFERENCE/DOCKET NUMBER: 31975
TELECOMMUNICATION INFORMATION:
TELEPHONE: (312) 474-6300
"E:EFAX: (312) 474-6448
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INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
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                            OCTATOGCCTCACACAAAAACACAAAGACAAGTTCTTTCCCATGAGCGGTGTCATGATT 1020
3706 TGGACTGGAGCTACCAAGTACCACCTCAATGGCAGAGACTCTCTGGTGAATCCGGGGCCC 3765
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Search completed: November 29, 2005, 14:27:50 Job time: 233.137 secs

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       The patent discloses an adeno-associated virus serotype 1 (AAV-1) DNA
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Add0772 Adeno-ass
Add75507 Adeno-ass
Add75507 Adeno-ass
Add39758 AAV-1 gen
Adz26931 Adeno-ass
Adz26930 Adeno-ass
Adz26932 Adeno-ass
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                          GenCore version 5.1.6 (c) 1993 - 2005 Compugen Ltd.
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which is characterised by two inverted terminal repeats (ITR) and open reading frames for rep and capsid (cap) proteins. The rep reading frame encodes four proteins, Rep 78, Rep 68, Rep 52 and Rep 40, while the cap reading frame encodes three structural proteins, VP1, VP2 and VB3. The AAV-1 sequence or its fragments particularly ITRs, rep and cap coding regions, are useful in production of recombinant viral vectors for gene delivery. These vectors can be used as gene therapy vectors, vaccine vectors or antisense delivery vectors. The AAV-1 does not induce the formation of neutralising antibodies specific to any serotype of AAV mace is useful for transforming host cells, and in the preparation of a medicament for the delivery of transgene to a host. The present sequence is an AAV-1 DNA encoding a cap protein VP3 which is useful in the production of recombinant viral vector for gene delivery
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TITAGCCGTGGGTCTCCAGCTGGCTGTTCAGCCCAAAAACTGGCTACCTGGACCC
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preparation of medicament for delivery of a transgene to a host.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              The patent discloses an adeno-associated virus serotype 1 (AAV-1) DNA which is characterised by two inverted terminal repeats (ITR) and open reading frames for rep and capsid (cap) proteins. The rep reading frame encodes four proteins, Rep 78, Rep 68, Rep 52 and Rep 40, while the cap reading frame encodes three structural proteins, VP1, VP2 and VP3. The AAV-1 sequence or its fragments particularly ITRs, rep and cap coding regions, are useful in production of recombinant viral vectors for gene continuous transfers of the sectors or antisense delivery vectors. The AAV-1 does not induce the formation of neutralising antibodies specific to any serotype of AAV hence is useful for transforming host cells, and in the preparation of medicament for the delivery of transgene to a host. The present sequence is an AAV-1 DNA encoding a cap protein VP1 which is useful in the production of recombinant viral vector for gene delivery
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preparation of medicament for delivery of a transgene to a host.
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Matches 1604; Conservative 0; Mismatches 0; Indels 0;
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                                                            GAGCCTCGCCCCATTGGCACCGTTACCTTACCGTCCCCTGTA 1604
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The invention relates to an adeno-associated virus (AAV) clade comprising at least three AAV members, where each member of the AAV clade is phylogenetically related as determined using a Neighbor-Joining heuristic by a bootstrap value of at least 75 % per 1000 isolates and a Polsson correction distance measurement of no more than 0.05. The methods and compositions of the present invention are useful for the prevention and/or treatment of fheumatoid arthritis, multiple sclerosis, asarcoidosis, diabetes, scleroderma, psoriasis, vasculitis, Crohn's disease, hemophilia, HIV, bacterial infection, cancer and ulcerative colitis. The present sequence represents an adeno-associated virus DNA.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                rheumatoid arthritis; multiple sclerosis; sarcoidosis; diabetes; scleroderma; psoriasis; vasculitis; Crohn's disease; hemophilia; HIV; bacterial infection; cancer; ulcerative colitis; antirheumatic; antiarthritic; neuroprotective; antiinflammatory; antidiabetic; antipporiatic; vasotropic; gastroincestinal-gen.; hemostatic; anti-HIV; virucide, antibacterial; cytostatic; antiulcer; dermatological; ds.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                       The invention relates to an adeno-associated virus (AAV) clade comprising at least three AAV members, where each member of the AAV clade is phylogenetically related as determined using a Neighbor-Joining heuristic by a bootstrap value of at least 75 % per 1000 isolates and a Poisson correction distance measurement of no more than 0.05. The methods and compositions of the present invention are useful for the prevention and/or treatment of rheumatoid arthritis, multiple sclerosis, arcoldosis, diabetes, scleroderma, psorialisis, vasculitis, Crohn's disease, hemophilia, HIV, bacterial infection, cancer and ulcerative colitis. The present sequence represents an adeno-associated virus DNA.
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                                                                                                                                                                                                                                                                                                                                         members, useful for preventing and/or treating arthritis, multiple
sclerosis, diabetes, scleroderma, psoriasis, hemophilia, HIV, bacterial
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                                                                                                                                                                                                                                                                                                                      adeno-associated virus (AAV) clade comprising
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100.0%; Score 1604;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1604; Conservative 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                    Disclosure; SEQ ID NO 79; 569pp; English.
                                                                                                                                                                                                                                         Alvira MR,
                                                                                                                                         2003US-0508226P.
2004US-0566546P.
                                                                                                    30-SEP-2004; 2004WO-US028817
                                                                                                                                                                                                  (UYPE-) UNIV PENNSYLVANIA
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                                                                                                                                         30-SEP-2003;
29-APR-2004;
                                                             14-APR-2005
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                                      TCCAATTATGCAAAATCTGCCAACGTTGATTTTACTGTGGACAACAATGGACTTTATACT
1387 TTTAGCCGTGGGTCTCCAGCTGGCATGTCTGTTCAGCCCAAAAACTGGCTACCTGGACCC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    The invention relates to a novel recombinant herpes simplex virus (rHSVS) whose genome is respectively inserted by the Adeno-associated virus (AAV) rep gene and cap gene. The AVV genes may be derived from viruses AAVI, AAV2, AAV3, AAV4, AAV5 and AAV6. The methods of the invention may be useful for generating recombinant vectors with high efficiency and no need of reconfiguration. The current sequence is that of the Adeno-associated virus 2 (AAV2) rep-Adeno-associated virus 1 (AAV1) cap fusion
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            2867 TTTGATTTCAACAGATTCCACTGCCACTTTTCACCACGTGACTGGCAGCGAGCTCATCAAC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 4347 BP; 1106 A; 1186 C; 1142 G; 913 T; 0 U; 0 Other;
2167 GAGCCTCGCCCCATTGGCACCCGTTACCTTACCCGTCCCCTGTA 2210
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                                                                                                                                                                           genetically engineered microorganism; vector; rep; cap;
                                                                                                                                                                                                                                                                                                                                                                                                                                                 Structure of a recombinant herpes simplex virus and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        DB 13;
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100.0%; Score 1604;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1604; Conservative 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Claim 1; SEQ ID NO 1; 102pp; Chinese
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                                                                  ADW39398 standard;
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The invention relates to a recombinant herpes simplex virus (HSV)

Characterized in that its genome is inserted with a DNA sequence selected

Characterized in that its genome is inserted with a DNA sequence selected

from nucleotide sequences of ADZ46594 or their homologous

sequences. Also included are preparing the recombinant HSV (comprising

the construction of DNA fragments that contains sequences ADZ46594.

MDZ46599, and respectively inserting these 5 DNA fragments into genome of

HSV by applying genetic engineering to give the recombinant HSV), large-

scale production of 5 serotype recombinant adeno-associated viruses (AAV)

1, 3, 4, 5, and 6 (by preparing the recombinant HSV, establishing a one-

scream vector cell i.e. recombinant AAV vector cell-line, infecting the

corresponding vector cell-line with the 5 recombinant HSV in

recombinant AAV under the infective effect of the 5 recombinant HSV in

Che vector cell-line, separating and purifying the 5 serotype recombinant

AAV after lysing the AAV-containing cells and culture liquor to give a

crude lysate and further purification of rAAV by density-gradient

centrifugation or affinity chromatography) and a recombinant vector

Champing passing the AAV-containing ITR at both ends of AAV-1, AAV-3, AAV-4, AAV

containing the AAV-searly enhancer and promoter of

cytomegalovirus, and a polyclonal site and a polyA signal, respectively,

between the ITR (inverted terminal repeat), and neomycin-resistance gene-
 Genetic engineering; gene therapy; vector; cancer; neoplasm; cytostatic; respiratory disease; respiratory-gen.; neurological disease;
                                                                                                                          TCCAATTATGCAAAATCTGCCAACGTTGATTTTACTGTGGGACAACAATGGACTTTATACT
                                                       4067 ATTGAATGGGAGCTGCAGAAAAGAAAACAGCAAGCGCTGGAATCCCGGAAGTGCAGGACACA
                                                                                                        TCCAATTATGCAAAATCTGCCAACGTTGATTTTACTGTGGACAACAATGGACTTTATACT
                                    ATTGAATGGGAGCTGCAGAAAAAAAAAGCAGCAGCTGGAATCCCGGAAGTGCAGTACACA
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associated virus vectors by infecting cells with recombinant herpes
simplex virus vectors, for use in gene therapy of e.g. cancer and
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Human herpesvirus 1.
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Adeno-associated virus serotype 1; AAV-1; rep protein; capsid protein; cap protein; recombinant viral vector; gene delivery; gene therapy;
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       into Xbal site in UL2 or UL44 gene in HSV genome. The DNA sequence of sequence ADZ46594-ADZ46598 can also be inserted into other non-essential gene regions in HSV genome. The recombinant HSV is optionally inserted with other DNA sequences homologous with the already-specified fragments. The vectors are for use in gene therapy of e.g. cancer, respiratory diseases and neural diseases. The virus vectors are safe, with long expression time and wide-spectrum of cell infection, even non-cleaved cells and reverse axonal conduction through the incorporated HSV vectors, and high transfer efficiently. The present sequence is the HSV-AAV sequence rep2cap1 for the AAV/HSV vectors of the invention.
expressing cassette at outer edge of ITR). The DNA sequence is inserted
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Best Local Similarity 100.0%; Pred. No. 0;
Matches 1604; Conservative 0; Mismatches 0; Indels 0;
                                                                                                                                                              Sequence 4347 BP; 1106 A; 1186 C; 1142 G; 913 T; 0 U; 0 Other;
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2889 AATGCCTCAGGAAATTGGCATTGCGATTCCACATGGCTGGGCGACAGAGTCATCACCACC 2948
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   241 TITGATITCAACAGATICCACTGCCACTITICACCACGTGACTGGCACGACTCATCAAC 300
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           The present sequence is an adeno-associated virus serotype 1 (AAV-1) DNA characterised by two inverted terminal repeats (ITR) and open reading frames for rep and capsid (cap) proteins. The rep reading frame encodes four proteins, Rep 78, Rep 68, Rep 52 and Rep 40, while the cap reading frame encodes three structural proteins, VP1, VP2 and VP3. The AAV-1 sequence or its fragments particularly ITRs, rep and cap coding regions, are useful in production of recombinant viral vectors for gene delivery. These vectors can be used as gene therapy vectors, vaccine vectors or antisense delivery vectors. The AAV-1 does not induce the formation of neutralising antibodies specific to any serotype of AAV hence is useful for transforming host cells, and in the preparation of a medicament for the delivery of transgene to a host
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      2949 AGCACCCGCACCTGGCCCTTGCCCACAATAACCACCTCTACAAGCAAATCTCCAGT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  181 GCTTCAACGGGGGCCAGCAACGACACCACTACTTCGGCTACAGCACCCCCTGGGGGTAT
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                                                                                                    /*tag= v
/label= 3'_ITR
/note= "inverted terminal repeat which is capable of
forming T-shaped hairpin structure"
                                                                                                                                                                                                                                                                                                                                                                                              WPI; 2000-376571/32.
P-PSDB; AAY71161, AAY71164, AAY71165, AAY71166, AAY71167, AAY71168,
                                                                                                                                                                                                                                                                                                                                                                                                                                                               Novel adeno-associated virus serotype 1 polynucleotide useful for preparation of medicament for delivery of a transgene to a host.
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100.0%; Pred. No. 0;
tive 0; Mismatches
          /note= "Capsid protein"
/note= "Capsid protein"
/+47. .4452
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.4718
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4576..4
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Best Local Similarity
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                                                   polyA_signal
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                                                                                    repeat_unit
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Rep 40"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 function= "regulates replication and integration of AAV NAA into host cell's chromosome" note= "The coding region is interrupted by intron"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            '*tag= n
product= "Rep 52"
function= "regulates replication and integration of AAV
NA into host cell's chromosome"
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                 ğ
label= 5' ITR
'note= "Inverted terminal repeat which is capable
'orming T-shaped hairpin structure"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ONA into host cell's chromosome"
857. .862
                                                                                                                      *tag= c
note= "Terminal resolute site
                                                                   '*tag= b
'bound moiety= "Rep protein"
[24. .]25
                                                                                                                                                                                                                                                                                                           bound moiety= "YY1 factor" 70. .275
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/product= "VP1 protein"
/note= "Capsid protein"
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label= P19_TATA_Box
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label= P40_TATA-BOX
875. .1876
                                                                                                                                                                                  bound moiety= "USF"
note= "B box"
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label= P5_TATA-Box
                                                                                                                                                                                                                                                                                                                                                                                              *tag= h
note= "YY1/p5 RNA"
                                                                                                                                                                                                                                       *tag= e
label= P5_promoter
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                                                                                                                                                                                                                                                                                                                                                                                                                                                               product= "Rep 68"
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/*tag= m
/note= "P19 RNA"
1007. .2272
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note= "P40 RNA"
924. .2220
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/*tag= h
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2829. .44
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The invention relates to a novel method for detecting adeno-associated virus (AAV) sequences in a sample, which comprises subjecting a sample containing a DNA to amplification via a polymerase chain reaction (PCR). The AAV sequence have the following activities: cytostatic, antithermatic, antithermic, antithermic, antithermic, antithermic, antithermic, antithermic, antithermic, antithermic, and antinflammatory. The AAV sequence can be used in gene therapy or as part of a vaccine to treat disorders. The method is useful in detecting and/or identifying AAV sequences may be used e.g. for preventing or treating hyperproliferative conditions such as cancers and psoriasis, and other autoimmune diseases like rheumatoid arthritis, multiple sclerosis, diabetes, autoimmune thyroiditis, scleroderma or Crohn's disease. This polynucleotide sequence therefores and AAV related DNA sequence of the invention.
                                                                                                                                                                                                                                                                                                                                                                              adeno-associated virus, AAV; cytostatic; antipsoriatic; antirheumatic; antiarthritic; neuroprotective; antidiabelic; antithyroid; dermatological; antiinflammatory; gene therapy; vaccine; hyperproliferative; cancer; psoriasis; autoimmune disease; rheumatoid arthritis; multiple sclerosis; diabetes; autoimmune thyroiditis; scleroderma; Crohn's disease; gene; ds.
                             4269 ATTGAATGGGAGCTGCAGAAAGAAAACAGCAAGCAGCTGGAATCCCGAAGTGCAGTACACA
                                                                          TCCAATTATGCAAATCTGCCAACGTTGATTTTACTGTGGACAACAATGGACTTTATACT
                                                                                                        4329 rccaarrargcaaarcrgccaacgrrgarrrracrgrggacaacaarggacrrraracr
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Detecting adeno-associated virus sequences in a sample, useful for preventing or treating hyperproliferative or autoimmune diseases, comprises subjecting a sample having a DNA to amplification via polymerase chain reaction.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 4718 BP; 1121 A; 1393 C; 1273 G; 931 T; 0 U; 0 Other;
                                                                                                                                                         GAGCCTCGCCCCATTGGCACCCGTTACCTTACCCGTCCCCTGTA 1604
                                                                                                                                                                                                                                                                                                                                                  SEQ ID
                                                                                                                                                                                                                                                                                                                                                  DNA,
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17-DEC-2001; 2001US-0341117P.
01-MAY-2002; 2002US-0377066P.
05-JUN-2002; 2002US-0386675P.
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                                                                                                                                                                                                                                                    ADE76507 standard;
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AACAATTGGGGGATTCCGGCCCCAAGAGACTCCAAACTCTTCAAACTCTTCAACATCCAAGTCAAG
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se; cytostatic; neuroprotective; antiinflammatory; gene therapy; expression construct; adeno-associated virus; integration efficiency element; inverted terminal repeat; integration; chromosome; cancer; lymphoma; leukemia; multiple myeloma; neuroblastoma; retinoblastoma; inflammatory disease; arthritis;
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disease an New expression construct comprising a nucleic acid sequence encoding adeno-associated virus integration efficiency element, useful for treating cancer e.g. lung cancer or colon cancer or inflammatory dise e.g. arthritis.

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Disclosure; SEQ ID NO 3; 62pp; English

The invention relates to an expression construct comprising a nucleic acid sequence encoding an adeno-associated virus integration efficiency element (AAV IEE), which is devoid of AAV inverted terminal repeats (AAV IRE) and site-specifically integrates into a host cell chromosome when provided to the host cell in conjunction with an AAV Rep protein. The cypression construct can be used as a therapeutic factor for treating a mammal for a pathologic state which is cancer, including lung cancer, colon cancer, renal cancer, panal cancer, including lung cancer, cancer, bone cancer, barain cancer, bile duct cancer, bladder cancer, gastrointestinal cancer, laryngeal cancer, cervical cancer, gastrointestinal cancer, laryngeal cancer, prostatic cancer, retinoblastoma, ovarian cancer, prostatic cancer, thymus cancer thyroid cancer. Other pathologic state includes inflammatory disease (arthritis), neurodegenerative decreased a disease of an organ attributed to the presence of increased or decreased level of a particular gene product(s). This sequence

Sequence 4718 BP; 1121 A; 1393 C; 1273 G; 931 T; 0 U; 0 Other;

Gaps Length 4718; ö Indels DB 10; ö 100.0%; Score 1604; llarity 100.0%; Pred. No. 0; Conservative 0; Mismatches Query Match Best Local Similarity Matches 1604; Conserv

2888 2948 3008 3068 3248 3308 3368 300 240 360 420 480 540 900 120 180 TTTGATTTCAACAGATTCCACTGCCACTTTTCACCACGTGACTGGCAGCGACTCATCAAC AACAATTGGGGATTCCGGCCCAAGAGACTCAACTTCAAACTCTTCAACATCCAAGTCAAG GTCTTCTCGGACTCGGAGTACCAGCTTCCGTACGTCCTCGGCTCTGGCGCACCAGGGCTGC crecercegracegeses en contra co AATGGCAGCCAAGCCGTGGGACGTTCATCCTTTTACTGCCTGGAATATTTCCCTTCTCAG AGCACCCGCACCTGGGCCTTGCCCCACCTACAATAACCACCTCTACAAGCAAATCTCCAGT GCTTCAACGGGGCCAGCAACGACAACACTACTTCGGCTACAGCACCCCCTGGGGGTAT TITGATITICAACAGATICCACTGCCACTITICACCACGTGACTGGCAGCGACTCAAC GAGGICACGACGAATGATGGCGTCACAACCATCGCTAATAACCTTACCAGCACGGTTCAA **AATGCCTCAGGAAATTGGCATTGCGATTCCACATGGCTGGGCGACAGAGTCATCACCACC** GTCTTCGGACTCGGAGTACCAGCTTCCGTACGTCCTCGGCTCTGCGCACCAGGGCTGC CCCTCCGTTCCCGGCGGACGTGTTCATGATTCCGCAATACGGCTACCTGACGCTCAAC ATGCCTTCAGGCGCTGCCGCACCCAATGGCAGACAATAACGAAGGCGCCGACGGAGTGGGT AGCACCCGCACCTGGGCCTTGCCCACCTACAATAACCACCTCTACAAGCAAATCTCCAGT t 2829 2889 121 2949 3009 3069 3129 361 3249 3309 H 541 61 181 241 301 3189 421 481 g 8 g g g ò g ò ద 셤 δ ò ઠે 8 셤 δ ઠે ઠે

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ADG39758 ID ADG39758 standard; DNA; 4718

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3608 900 720 840 3849 TTTGGAAAAGAGGGCCGGAGCTTCAAACACTGCATTGGACATGTCATGATAACAGC CCTGGCATGGTGTGGCAAGATAGAGACGTGTACCTGCAGGGTCCCATTTGGGCCCAAAATT regacregrecricaaaararaacereaareegeereaareeareareaacereecae gerargocercacaaaagacgaagacaagrierrreecargaggergreatarr 3909 GAAGAGGAAATTAAAGCCACTAACCCTGTGGCCACCGAAAGATTTGGGACCGTGGCAGTC AATTTCCAGAGCAGCACACACACACCCTGCGACCGGAGATGTGCATGCTATGGGAGCATTA CCTCACACAGATGGACACTTTCACCCGTCTCCTTTATGGGCGGCTTTGGACTCAAGAAC CCGCCTCCTCAGATCCTCATCAAAAACACGCCTGTTCCTGCGAATCCTCCGGCGGAGTTT 4149 CCGCCTCCTCAGATCTCCAGAAAAAAACACGCCTGTTCCTGCGAATCCTCCGGCGGGAGTTT ATTGAATGGGAGCTGCAGAAAAAAAAACAGCAAAGCGCTGGAATCCCGAAGTGCAGTACACA TCCAATTATGCAAAATCTGCCAACGTTGATTTTACTGTGGACAACAATGGACTTTATACT 1329 TCCAATTATGCAAATCTGCCAACGTTGATTTTACTGTGGACAACAATGGACTTTATACT AGCAGCTACGCGCACAGCCCAGAGCCTGGACCGGCTGATGAATCCTCTCATCGACCAATAC CTGTATTACCTGAACAGAACTCAAAATCAGTCCGGAAGTGCCCAAAACAAGGACTTGCTG CTGTATTACCTGAACAGAACTCAAAATCAGTCCGGAAGTGCCCAAAACAAGGACTTGCTG TTTAGCCGTGGGTCTCCAGCTGGCATGTCTGTTCAGCCCAAAAACTGGCTACCTGGACCC TGTTATCGGCAGCAGCGCGTTTCTAAAACAAAACAGACAACAACAACAGCAATTTTACC TGGACTGGTGCTTCAAAATATAACCTCAATGGGCGTGAATCCATCATCAACCCTGGCACT GCTATGGCCTCACACAAGACGACGAGGACAAGTTCTTTCCCATGAGCGGTGTCATGATT TTTGGAAAAGAGGCCCCGGAGCTTCAAACACTGCATTGGACAATGTCATGATTACAGAC GAAGAGGAAATTAAAGCCACTAACCCTGTGGCCACCGAAAGATTTGGGACCGTGGCAGTC TTTAGCCGTGGGTCTCCAGCTGGCATGTTCAGCCCAAAAACTGGCTACCTGGACCC 4432 GAGCCTCGCCCCATTGGCACCCGTTACCTTACCGTCCCCTGTA 1604 GAGCCTCGCCCCATTGGCACCCGTTACCTTACCCGTCCCCTGTA 3969 4209 4269 3429 3489 3549 3609 3669 3729 3789 1021 1081 1141 1201 4029 1261 4089 1321 1381 1441 1501 1561 4389 781 841 901 661 721 961 601

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3849 TTTGGAAAAGAGGGCGCGGAGCTTCAAACACTGCATTGGACAATGTCATGATTACAGAC 3908
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                                        2949 AGCACCCGCACCTGGGCCTTGCCCACCTACAATAACCACCTCTACAAGCAAATCTCCAGT
                                                                                                                    3009 GCTTCAACGGGGGCCACCAACGACAACCACTACTACAGCTACAGCACCCCCTGGGGGTAT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  The present invention describes a polynucleotide (1), comprising
rep coding sequences and parvovirus cap coding sequences. The
rep coding sequences encodes a DNA binding domain from a first ferent
parvovirus, and a capsid interacting domain from a parvovirus different
from the first parvovirus. The cap coding sequence comprises sequences
from the different parvovirus. Also described: (1) a vector comprising
(1), (2) a cell comprising (1), or parvovirus rep coding sequences and
parvovirus cap coding sequences, where the rep coding sequences encode a

CC (1), (2) a cell comprise (1), or parvovirus encoding sequences and
parvovirus different from the first parvovirus, the cap
coding sequences are stably integrated into the genome of the
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coding sequences are stably integrated into the genome of the
stocks of hybrid parvoviruse or parvovirus vectors, which may be used in
coding sequences or parvovirus sector
coding sequences or parvovirus avector may also be used to produce a parvovirus vector
coding sequence in vivo, or in diagnostic and screening
coding sequence is used in the exemplification of the
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ATGCCTTCAGGCGGTGGCGCACCAATGGCAGACAATAACGAAGGCGCCGACGAAGGGGGT
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                                                                                                                              parvovirus; rep; cap; DNA binding domain; capsid interacting domain; recombinant hybrid parvovirus particle; recombinant adeno-associated virus; rAAV; AAV; vaccine; gene therapy;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Gaps
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Best Local Similarity 100.0%; Pred. No. 0;
Matches 1604; Conservative 0; Mismatches
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                                                                                              AAV-1 genomic DNA sequence SEQ ID NO:20
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                                                       (first entry)
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produced from pFBDAAV1-VP for use in the production of recombinant AAV particles comprising AAV1 capsid proteins in insect (Sf9) cells. The method of producing AAV in insect cells provides an efficient, safe and economical means of producing a large amount of recombinant AAV particles which may be used in gene therapy
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                                                                                                Sequence 7447 BP; 1870 A; 1934 C; 1795 G; 1848 T; 0 U; 0 Other;
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Matches 1604; Conservative
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                                                                                                                                                  CGCCTCCTCAGATCCTCATCAAAAACACGCCTGTTCCTGCGAATCCTCCGGGGGGGTTT
                                                                                                                                                                                        ATTGAATGGGAGCTGCAGAAAGAAAACAGCAAGCGCTGGAATCCCGAAGTGCAGTACACA
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                             CCTGGCATGGTGTGGCAAGATAGAGACGTGTACCTGCAGGGTCCCATTTGGGCCCAAAATT
                                                                     CCTCACACAGATGGACACTTTCACCCGTCTCCTTTATGGGCGGCTTTTGGACTCAAGAAC
                                                                                     CCTCACACACAGATGGACACTTTCACCCGTCTCCTTATGGGCGGCGTTTGGACTCAAGAAC
          CCTGGCATGGTGGCAAGATAGAGACGTGTACCTGCAGGGTCCCATTTGGGCCCAAAATT
                                                                                                                                CCGCCTCCTCAGATCCTCATCAAAACACGCCTGTTCCTGCGAATCCTCCGGCGGAGTTT
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13-AUG-2002; 2002US-00216870.
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                                                                                                                                                                                                                                                                The invention relates to an adeno-associated virus (AAV) clade comprising at least three AAV members, where each member of the AAV clade is phylogenetically related as determined using a Neighbor-Joining heuristic by a bootstrap value of at least 75 % per 1000 isolates and a Poisson correction distance measurement of no more than 0.05. The methods and compositions of the present invention are useful for the prevention and/or treatment of rheumatoid arthritis, multiple sclerosis, sarcoidosis, aclaroderma, psoriasis, wasculitis, Crohn's dispets, scleroderma, psoriasis, vasculitis, Crohn's dispease, hemophilia, HIV, bacterial infection, cancer and ulcerative colitis. The present sequence represents an adeno-associated virus DNA.
                                                                                                                                          members, useful for preventing and/or treating arthritis, multiple sclerosis, diabetes, scleroderma, psoriasis, hemophilia, HIV, bacterial infection and cancer.
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                                                                                     Vandenberghe LH;
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Pred. No. 0;
0; Mismatches
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                                                                                     Alvira MR,
   30-SEP-2003; 2003US-0508226P.
29-APR-2004; 2004US-0566546P.
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Best Local Similarity 99.9%;
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New adeno-associated virus (AAV) clade comprising at least three AAV members, useful for preventing and/or treating arthritis, multiple sclerosis, diabetes, scleroderma, psoriasis, hemophilia, HIV, bacterial infection and cancer.
                                                                                                rheumatoid arthritis; multiple sclerosis; sarcoidosis; diabetes; scleroderma; psoriasis; vasculitis; Crohn's disease; hemophilia; HIV; bacterial infection; cancer; ulcerative colitis; antiheumatic; antiarthritic; neuroprotective; antiinflammatory; antidiabetic; antiarthripsoriatic; vasorropic; gastrointestinal-gen.; hemostatic; anti-HIV; virucide; antibacterial; cytostatic; antiulcer; dermatological; ds.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           The invention relates to an adeno-associated virus (AAV) clade comprisi at least three AAV members, where each member of the AAV clade is phylogenetically related as determined using a Neighbor-Johingh heurist by a bootstrap value of at least 75 % per 1000 isolates and a Poisson correction distance measurement of no more than 0.05. The methods and compositions of the present invention are useful for the prevention and/or treatment of rheumatoid arthritis, multiple sclerosis, esarcoidosis, diabetes, scleroderma, psoriasis, vasculitis, Crohn's disease, hemophilia, HIV, bacterial infection, cancer and ulcerative colitis. The present sequence represents an adeno-associated virus DNA.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       rheumatoid arthritis, multiple sclerosis; sarcoidosis; diabetes; scleroderma; psoriasis; vasculitis; Crohn's disease; hemophilia; HIV; bacterial infection; cancer; ulcerative colitis; antirheumatic; antiarthritic; neuroprotective; antilfammatory; antidiabetic; antipsoriatic; vasotropic; gastrointestinal-gen; hemostatic; anti-HIV; virucide; antibacterial; cytostatic; antiulcer; dermatological; ds.
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2050 ATTGAATGGGAGCTGCAGAAAQAAAACAGCAAGCGCTGGAATCCCGAAGTGCAGTACACA
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Wilson,J.M. and Xiao,W.
Adeno-associated virus serum type 1 nucleic acid sequence, vector and host cell containing the same
Patent: JP 200229098+A 8 10-SEP-2002;
THE TRUSTEES OF THE UNIVERSITY OF PENNSYLVANIA
                                                                                                                                                                                                                                                                                                                                             BD242773
Adeno-associated virus serum type 1 nucleic acid sequence, vector and host cell containing the same.
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Best Local Similarity 100.0%; Pred. No. 0;
Matches 1604; Conservative 0; Mismatches
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JP 2002529098-A/8
10-SEP-2002
02-NOV-1999 JP 2000581227
05-NOV-1998 US 60/107114
JAMES M WILSON, WEIDONG XIAO
                                                                                                                                                                                                                                                                                              ALIGNMENTS

    1605
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/mol_type="genomic DNA"
/db_xref="taxon:32644"

                                                         AF028704

AY330567

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CS073448

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AR562504 Sequence
BD242771 Adeno-ass
CS073491 Sequence
CS073491 Sequence
AR562503 Sequence
BD242766 Adeno-ass
AR562498 Sequence
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AR663497 Adeno-ass
AR663497 Adeno-ass
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                                                                     November 28, 2005, 12:51:27; Search time 5861.51 Seconds (without alignments) 15555.198 Million cell updates/sec
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                                                                                                                                  1 atggcttcaggcggtggcgc......taccttacccgtccctgta 1604
            GenCore version 5.1.6 (c) 1993 - 2005 Compugen Ltd.
                                                                                                                                                                                    5883141 seqs, 28421725653 residues
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Listing first 45 summaries
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Result Š.

1081 GAAGGAAATTAAAGCCACTAACCCTGTGGCCACCGAAAGATTTGGGACCGTGGCAGTC	Db 1141 AATTCCAGAGCAGCAGCACCCTGCGACCGAGAGATGTGCATGCGAGGAGTTA 1200 Qy 1201 CCTGGCATGGTGTGGCAAGATAGAGACGTGCTACCTGCAGGGTCCCATTTGGGCCAAAATT 1260 Db 1201 CCTGGCATGGTGGCAAGATAGAGACGTGTACCTGCAGGGTCCCATTTGGGCCAAAATT 1260	1261 CCTCACACAGATGACACTTTCACCCGTCTCCTTATGGGCGGCTTTGGACTCAAGAAC	1321 CGCCTCCTCAGATCAAAAACACGCCTGTTCCTGCGAATCCTCGGCGGGTTT 1321 CGCCTCCTCAGATCTCAAAAACGCCCTTTCCTGCGAATCCTCCGGCGGGGTTT 1321 CGCCTCCTCAGATCCTCAAAAACGCCTGTTCCTGCGAATCCTCCGGCGGGGGTTT	1381 TCAGCTACAAAGTTTGCTTCATCACCCAATACTCCACAAGGACAAGTGAATGAA	1441 ATTGATTGGGAGTGCAGAAACAACAACTGGAATTCCCGAAGTTGCAGTTCCAG 1 1441 ATTGAATGGGAGCTGCAGAAAGAAAACACAAGCAAGCTGGAAGTGCAGTGCACA 1	1501 TCCAATTATGCAAAATCTGCCAAGGTTGATTTTACTGTGGACAA	Db 1561 GAGCCTCGCCCATTGGCACCGTTACCCCCTGTA 1604 Db 1561 GAGCCTCGCCCCATTGGCACCCGTTACCCTGTA 1604	RESULT 2 AR562505 AR562505 AR562505 1605 bp DNA linear PAT 08-OCT-2004 DEFINITION cancents 16 from natent 115 6750337	AR562505.1 GI:53976571	NISM	TITLE Adeno-associated virus serotype 1 nucleic acid sequences, vectors and host cells containing same JOURNAL Patent: US 6759237-A 16 06-701-2004; The Trippess of the Inviscity of Benneylyanis: Dhiladelphia Da	ī	ORIGIN Query Match Query Match 100.0%; Score 1604; DB 6; Length 1605;	best Local Similarity 100.0%; Fred. No. 0; Matches 1604; Conservative 0; Mismatches 0; Indels 0; Gaps 0; Ox 1 ATGCTTCAGGCGACGACGACCACCAATGACAAAAAGAAAG	1	Qy 61 AATGCCTCAGGAAATTGGCATTGCGATTCCACATGGCTGGGCGACAGACTCATCACCACC 120 Dh 61 AATGCCTCAGGAAATTGGCATTCCACATGCGCGACAGAGTCACCACCACCACCACCACCACCACCACCACCACCACCAC	121 AGCACCGCACCTTGCCCACCTACAATAACCACCTTACAAGCAAATCTCCAGT
TTCAGGCGGTGGCACCAATGGCAGACAATAACGAAGGCGCCGACGGAC 	61 AATGCCTCAGGAAATTGGCATTGCGATTCCACATGGCTGGGGGGTCATCACCACC 120 121 AGCACCCGCACCTGGGCCTTGCCCACCTACACACACACAAGAAATCTCAGT 180 121 AGCACCCGCACCTTGGCCACCTACACAATAACCACCTCTACAAAGAAATCTCCAGT 180 121 AGCACCCGCACCTTGGCCACCTAGCCACACACAAATCTCCAGT 180	GCTTCAACGGGGCCAGCAACGACACCACTACTTCGGCTACAGCACCCCCTGGGGGTAT 	241 TTTGATTTCAACAGATTCCACTGCCACTTTTCACCACGTGACTGGCAGCGACTCATCAAC 300 	301 AACAATTGGGGATTCCGGCCCAAGAGACTCAACTTCAAACTCTTCAAACATCCAAGTCAAG 360 	OY 361 GAGGTCACGACGAATGATGCGTCACCATCGCTAATAACCTTACCAGCACGGTTCAA 420	dy 421 GPCTTCTCGGAGTCCGAGCTTCCGTACGTCCTCGGCTCTGCGCACCAGGGCTGC 480 bb 421 GPCTTCTCGGAACTCGGAGTACCAGCTTCCGTACGTCGTCGGCTCTGGCGCACCAGGGTGC 480	Qy 481 CTCCCTCCGTTCCCGGGGGACGTGTTCATGATTCCGCAATACGGCTACCTGACGTCCAAC 540 Db 481 CTCCCTCCGTTCCCGGGGGACGTGTTCATGATTCCGCAATACGGCTACCTGACGTCCAAC 540	dy 541 AATGGCAGCCAAGCCGTGGGACGTTCATCCTTTACTGCCTGGAATATTTCCCTTCTCAG 600 Db 541 AATGGCAAGCCAAGCCGTGGAACGTTCATCCTTTTACTGCCTGGAATATTTCCCTTCTCAG 600	OY 601 AIGCIGAGAACGGCAACAACTITACCTICAGCTACACCTTTGAGGAAGIGCCTTTCCAC 660	dy 661 AGCAGCTACGCGCACAGCCCGGACCGGCTGATGAATCCTCTCATCGACCAATAC 720 	OY 721 CIGIATTACCTGAACAGAACTCAAAATCAGTCCGGAAGTGCCCAAAAGAGACTTGCTG 780	Qy 781 TTTAGCCGTGGGTCTCCAGCATGTCTGTTCAGCCCAAAAACTGGCTACCTGGACCC 840 Db 781 TTTAGCCGTGGGTCTCCAGCTGGCATGTCTGTTCAGCCCAAAAACTGGCTACCTGGACCC 840	OY 841 TGTTATCGGCAGCAGCGCTTTCTAAAACAAAAACAAAAAAAA	Qy 901 TGGACTGGTGCTTCAAAATATAAACCTCCAATGGGCGTGAATCCATCATCATCAGCACT 960 Db 901 TGGACTGGTGCTTCAAAATATAACCTCAATGGGCGTGAATCCATCATCATCAGCACT 960	961 GCTATGCCTCACAAAGACGACGAAGACAACTTCTTTCCATGAGCGGTGTCATGATT	Db 961 dcTATGGCCTCACAAAGACGACGAAGACAAGTTCTTTCCCATGAGCGGTGTCATGATT 1020 Ov 1021 TTTGGBABAGAGAGGGCGGCGAAGTTTCBARAATGAAGAAGTTGAAAAGAGAAGATGAAAGAGTGATGAAGAGATTAAAAGAG 1080	1021 TITGGAAAGGGCCGGAGCTTCAAACACTGCATTGGACATGTCATGATTACAGAC

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2 Milson,J.M. and Xiso,W.

2 Meno-associated virus serum type 1 nucleic acid sequence, vector and host cell containing the same
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THE TRUSTEES OF THE UNIVERSITY OF PENNSYLVANIA
OS AAV-1

PN NP 202529098-A/7

PP 10-SEP-2002

PP 02-NOV-1999 JP 2000581227

PR 05-NOV-1999 US 60/107114

PI JAMES M MILSONG XIAO

PC C12N15/09,A61X31/711,A61X48/00,A61P43/00,C12N1/15,C12N1/19, PC
C12N1/21,
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                                  1261 CCTCACACAGATGGACACTTTCACCCGTCTCCTTATGGGCGGCTTTGGACTCAAGAAC
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                                                                                                     CCGCCTCCTCAGATCCTCATCAAAACACGCCTGTTCCTGCGAATCCTCCGGCGGAGTTT
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/organism="unidentified"
/mol_type="genomic DNA"
/db_xref="taxon:32644"
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AUTHORS Wilson,J.M. and Xiao,W. TITLE Melbon,J.M. and Xiao,W. TITLE and host cell containing the same JOURNAL PREENT: JP 2002529098-A 1 10-SEP-2002; PR TRUSTEES OF THE UNIVERSITY OF PENNSYLVANIA PN JP 2002529098-A/1 PN JP 2002529098-A/1 PN JP 2002529098-BN I DO SEP-2002 PP 02-NOV-1998 US PR 05-NOV-1998 US PR OS-NOV-1998 US PC CTT
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BD242766 4718 bp DNA linear PAT 17-JUL-2003 Adeno-associated virus serum type 1 nucleic acid sequence, vector

RESULT 9 BD242766 LOCUS DEFINITION

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Milson, Am. and Xiao, W.
Adeno-associated virus serotype 1 nucleic acid sequences, vectors and host cells containing same
and host cells containing same
Patent: US 6759237-A 1 06-UUL-2004;
The Trustees of the University of Pennsylvania; Philadelphia, PA
Location/Qualifiers
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/ COGOD. BESTE=1
/ Product="nortural protein"
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/ product="nortural protein"
/ protein_id="AAD27758.1"
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TKSARAPDYLVQPAPPADISTNRIYRIYRILELNGYEPAYAGSVFLGWAQKRRNTIWLFG
PATTGKTNIAEAIAHAVPFYGCVNWTNENFPRDCVDKWVIWHEGGKMTAKVVSSAKA
ILGGSKRAVDQKCKSSAQIDPTPVIVTSNTNMCAVIDGNSTTFEHQOPLQDBWEKFEL
TRRLEHDFGKYTKOGVKEFFRWAQDHVTEVAHEFYVRKGGANKRPAPDDADKSBFRA
TRRLEHDFGKYTKOGSARAPRYQNKCSRHAGMLQWLFPCKTCSRMNONFNICFTHGT
RCSECFFGVSSGQPVVRKRTYRKLCAIHHLLGRAPEIACSACDLVNVDLDDCVSEQ"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               STPMOTEDERMEHCHESPENDMOTELINNWHERERENEELEN LOVEETTINDGVTTIA
NULTSTVQVESDESTVQLPYLGSAHQCCLPPPRADVEMI POYGYLTTINGGOAVGRSS
NULTSTVQVESDESTVQLPYLGSAHQCCLPPPRADVEMI POYGYLTILNNGSQAVGRSS
NQSGBAQNKDLLFSSTFESTFESTPSSTPSSTANDSVEMINDLFLDVLYLINNTG
NQSGBAQNKDLLFSGSPSOPATHOPPRAGOYMI FORESAGASNTALDNVMI TDEEEI
TATNVATERETGTVANNSGSSTDPATGDVHAMAALDEWVMODRDVYLLQGPI MAKT PH
TDGHTHPSPLMGGGCLINNPPROPI LI KNTPVPANPPREFSSATKRASFT TQYSTGQVSVE
I EWELQKENSKRWNPEVQYTSNYAKSANVDFTVDNNGLYTEPRP PI GTRYLTRPL"
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LVLPGYKYLGPFNGLDKGBEWNAADAALEHDKAYDOQLKAGDNPYLRYNHADAEFOB
RLQBDTSFGGNLGRAVFQAKKRVLPELGLVEEGAKTAPGKKRPVEGSPGEPDSSSGIG
KTGQQPAKKRLNFGGTGDSESVPDPQPLGEPPATPANOBTTWASGGGAPMADNNBGA
DGVGNASGNWHCDSTWLGDRVITTSTRTWALPTYKQISSAGTGASNDNYFGY
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Submitted (05-MAY-1998) IHGT, University of Pennsylvania, 3601
Spruce Street, Philadelphia, PA 19104, USA
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ATGGCTTCAGGCGCTGGCGCACCAATGGCAGACAATAACGAAGGCGCCGACGGAGTGGGT
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                                                                                  /organism="Adeno-associated virus 1"
/mol_type="genomic DNA"
/db_xref="taxon:85106"
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Pred. No. 0;
); Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /product="capsid protein"
/protein_id="AAD27757.1"
/db_xref="GI:4689097"
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Best Local Similarity 100.0%; P:
Matches 1604; Conservative 0;
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                                                 8669 IGITATCGGCAGCAGCGCGTITCTAAAACAAAAACAACAACAACAACAACAACAATITIACC 3728
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Adeno-associated virus 1
Viruses; ssDNA viruses; Parvoviridae; Parvovirinae; Dependovirus.
1 (bases 1 to 4718)
Xiao,W., Chirmule,N., Berta,S.C., McCullough,B., Gao,G. and Wilson,J.M.
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                                                                                                                                                                                                                                     GCTATGGCCTCACACAAGACGACGAGACAAGTTCTTTCCCATGAGCGGTGTCATGATT
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                                                                                                                                                                                             GCTATGGCCTCACACAAAGACGACGAAGACAAGTTCTTTCCCATGAGCGGTGTCATGATT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CCTGGCATGGTGTGGCAAGATAGAGACGTGTACCTGCAGGGTCCCATTTGGGCCAAAATT
                                                                                                          TGGACTGGTGCTTCAAAATATAACCTCAATGGGCGTGAATCCATCATCAACCCTGGCACT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            AATTTCCAGAGCAGCACACACACCCTGCGACCGGAGATGTGCATGCTATGGGAGCATTA
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J. Virol. 73 (5), 3994-4003 (1999)
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AF063497.1 GI:4689096
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Xiao, W. and Wilson, J.M.
Direct Submission
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Db 4269 ATTGAATGGAAGAGAAAAGAAAACAGCAAGGAATCCCGAAGTGCAGTACAC 4328 Qy 1501 TCCAATTATGCAAATTTGCCAACGTTGATTTTACTGTGGACATAGACTTTATACT 1560 Bb 4329 TCCAATTATGCAAAATCTGCCAACGTTGATTTTACTGTGGACAAATGGACTTTATACT 1580 Qy 1561 GAGCCTCGCCCCATTGGCACCCGTTACCTTACCCGTCCCCTGTA 1604	13 92 92 TION ION N	SOURCE Unknown. ORGANISM Unknown. REFERENCE 1 (bases 1 to 7447) AUTHORS Kotin,R.M., Urabe,M. and Ding,CT. TITLE Production of adeno-associated virus in insect cells JOURNAL Patent: US 6723551-A 11 20-APR-2004; The United States of America as represented by the Department of	Health and Human Services; Washington, DC FEATURES Location/Qualifiers 8 ource 1. 7447 /organism="unknown" /mol type="genomic DNA"		ss 1604; Conservative 1 ATGGCTTCAGGGGGGGGGG	Db 5227 ATGCTTCAGGCGTGGCGTCGCATGGCAGACATAACGAAGGCGCGACGAGTGGGTGG	Db 5287 AATGCCTCAGGAAATTGGCATTGCGATTGCGATGGCTGGGCGACAGAGTCATCACCACC 5346 Qy 121 AGACCCGACCTGGCCTTGCCCACAAAAAAAAAAAAAAAA	Db 5347 AGCACCGCACCTTGCCCTCTACATACCCTCTACAAGCAATCTCCAGT 5406 Qy 181 GCTTCAGGGGGCCCAGCAACCACCACCTACCTCGGCTACAGCACCCCCTGGGGGGTAT 240	Db 5407 GCTTCACGGGGCCACCCCACACACACTTCGGCTACACGCCCCCCCC	Db 5467 TITGATITTCAACAATTCCACTACTATTCACCACGTGACTGGCAGCGACTCAACAAC 5526 Oy 301 AACAATTGGGGATTCCGGCCCAAGAGACTCAACTTCAACTTCAAACTCTTCAAGTCAAG 360	Db 5527 AACAATTGGGGATTCCGGCCCAAGAGACTTCTAACTTCTAACATCTTCAAGATCTAAGAGTCAAG 5586 Qy 361 GAGGTCACGAGAATGGGGTCAACATCGCTAAAACTTAACGTTCAAGATCAAG 5586	Db 5587 GAGGTCCACGACGATGATGATGATCATCGTTATAACATGACGATCAGCAGGTTCAA 5646 Oy 421 GTCTTCTGGACTCCAGGTACCTACCAGGCTCTCGGCTCTCGGCTCTCGGCTCTCGGCTCTTCGGACTGCTTCGTACTTCTTCGTACTTCTTCTTCTTTTTTTT	5647	Db 5707 CTCCTCCGTTCCCGGGGGGGGGGTGTTCCGCAATACGGCTACCTCGACGCTCAAC 5766
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RESULT 14 CS073493 LOCUS DEFINITION Sequence 81 from Patent W0200503321. ACCESSION (S073493 CS073493 CS07349 CS073493 CS073493 CS07349 CS	Query Match Best Local Similarity 99.9%; Pred. No. 0; Matches 1602; Conservative 0; Mismatches 2; Indels 0; Gaps 0; Oy 1 Arggcrrcaggcgcacacacacacacacacacacacacaca	Db 607 Hidden 1 1 1 1 1 1 1 1 1	121 AGCACCTGGGCCTTGCCCACCTACANTAACCACTCTACAAGGAATCTCCAGT 180	Qy 181 GCTTCAACGGGGCCAGCAACGACAACTACTTCGGCTACACCCCCTGGGGGTT 240 Db 787 GCTTCAACGGGGCCAGCAACGACTACTTCGGCTACCTCGGGGGGTT 846	Qy 241 TTTGALTTCAACAGATTCCACTGCCACTTTTCACCACGGACTCATCAAC 300	Cy 301 AACAATTGGGGATTCCGGCCCAAGAGTCCACTTCAACTCTTCAACATCCAAGTCAAG 360	Qy 361 GAGGTCACGACGATGATGACGTCACAACCATCGCTAATAACCTTACCAGGGTTCAA 420 Db 967 GAGGTCACGACGATGATGGCGTCACAACCATCGCTAATAACCTTACCAGCACCACCACCATCACCATCAGCACCATCAACAACATACCTTACCAGCACCACCACAACAACAACAACAACAACAACAACAA	Qy 421 GTCTTCTCGGAGTACCAGCTTCCGTACGTCCTCGGCTCTGCGCACCAGGCTGC 480	Qy 481 CTCCTCCGTTCCCGGCGGACGTGTTCATGATTCCGCAATACGGCTACCTGACGCTCAAC 540	QY 541 AATGGCAGCCAAGCGTGGGAGCTTCATCCTTTTACTGCCTGGBATATTTCCCTTCTCAG 600 Db 1147 AATGGCAGCCAAGCCGTGGGACGTTCATCTTTTACTGCCTGGAATATTTCCCTTCTCAG 1206	Oy 601 ATGCTGAGAACACATTTACCTTCAGCTACACCTTTGAGGAAGTGCCTTTCCAC 660	G61 AGCAGCTACGCGCACAGCCTGGACCGGCTGATGAATCCTCTCATCGACCAATAC 720
Qy 581 AATGGCAGCCAAGCCGTGGACGTTCATCCTTTTACTGCCTGGAATATTTCCCTTCTCAG 600 Db 5767 AATGGCAGCCAAGCCGTGGAACGTTCATCCTTTTACTGCCTGGAATATTTCCCTTCTCAG 5826 Qy 601 ATGCTGAGAACGACAACATTTACCTTCAGCTACACCTTTGAGGAAGTGCCTTTCCAC 660 Db 5827 ATGCTGAGAACGGACAACATTTACCTTCAGCTACACCTTTGAGGAAGTGCCTTTCCAC 5886 Qy 661 AGCAGCTACGCGACAACAACTTTACCTTCAGCTACACCTTTGAGGAAGTGCCTTTCCAC 5886 Qy 721 CTGTATTACCTGAACAGCACAGCCTGAACGACGGCTGATGAATCCTCTCATCGACCAATAC 5946 Qy 721 CTGTATTACCTGAACAGAACTCAAAATCAGCCGGAAGTGCCCCAAACAACAAGCAGACTTGTTG 6006 Qy 721 CTGTATTACCTGAACAGAACTCAAAATCAGCCCGAAACAACAACAAGAACAAGAACAAGAACAAGAACAAGAACAAACAAGAACAAACAAGAACAAACAAGAACAAACAAGAACAAACAAGAACAAACAAACAAGAACAAACAAACAAACAAACAAACAAACAAACAAACAAACAAACAAACAAACAAACAAACAAACAAACAAACAAACAAAA	QY 901 TGGACTGGTGCTTCAAAATATAACCTCAATGGGGGTGAATCCATCATCAACCCTGGCACT 960 Db 6127 TGGACTTCAAAATATAACCTCAATGGGCGTGAATCCATCATCATCACCTTGGCACT 6186 QY 961 GCTATGGCCTCACACAAGACGAAGAAGACAAGTTCTTTCCCATGAGGGGGTGATGATT 1020	ν η ν	1081	1141	Qy 1201 CCTGGCATGGTGTGACAGATAGAGACGTGTACCTGCAGGGTCCCATTTGGGCCAAAATT 1260 Db 6427 CCTGGCATGGTGGCAAGATAGAGACGTGTACCTGCAGGGTCCCATTTGGGCCAAAATT 6486	0-0	Qy 1321 CCGCCTCCTCAGAICCTCATCAAAAACACGCCTGTTCCTGCGAATCCTCCGGGGGGGG	Qy 1381 TCAGCTACAAAGTTTGCTTCATCACCCAATACTCCACAGGACAAGTGAGTG	Qy 1441 ATTGAATGGGAGCTGCAGAAAAAACAGCAAGCGCTGGAATCCCGAAGTGCAGTACACA 1500 Db 6667 ATTGAATGGGAGCTGCAGAAAAAAAACAGCAAGCGCTGGAATCCCGAAGTGCAGTACACA 6726	Qy 1501 TCCAATTATGCAAAATCTGCCAACGTTGATTTTACTGTGGACAACAATGGACTTTATACT 1560	Qy 1561 GAGCCTCGCCCATTGGCACCGTTACCTTACCCTGTA 1604 Db 6787 GAGCTCGCCCCATTGGCACCGTTACCTTACCCTGTA 6830	

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         Viruses; SSDNA viruses; Parvoviridae; Parvovirinae; Dependovirus. 1 (bases 1 to 2211) (ac.6., Vandenberghe,L.H., Alvira,M.R., Lu,Y., Calcedo,R., Zhou,X. and Wilson,J.M. Clades of Adeno-associated viruses are widely disseminated in human
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                                                                                                                                            Gao, G., Vandenberghe, L.H., Alvira, M.R., Lu, Y., Calcedo, R., Zhou, X. and Wilson, J.M.

Direct Submission

Submitted (20-Jan-2004) Gene Therapy Program, Division of Medical Genetics, Department of Medicine, University of Pennsylvania, 3601 Spruce Street, Wistar Institute, Philadelphia, PA 19104, USA Location/Qualifiers
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/mol type="genomic DNA"
/isolate="hu.44"
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/db_xref="taxon:272636"
/country="USA"
/note="clade A"
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/protein_id="AAS9292.1"
/db_xref="G1:46487861"
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Db 1987 TCAGCTACAAAGTTTGCTTCJ Qy 1441 ATTGAATGGGAGCTGCAGAA Db 2047 ATTGAATGGGAGCTGCAGAAA Qy 1501 TCCAATTATGCAAAATCTGC Qy 1561 TCCAATTATGCAAAATCTGCC Qy 1561 GAGCCTCGCCCCATTGCCAC Db 2167 GAGCCTCGCCCCATTGCCAC	Search completed: November 29, 200: Job time : 5865.51 secs														
	541 AATGGCAGCCAAGCCGTGGGACGTTCATCCTTTTACTGCCTGGAATATTTCCCTTCTCAG 600	601 ATGCTGAGAACGGGCAACTTTTACCTTCAGCTACACCTTTGAGGAAGTGCCTTTCCAC 660 1207 ATGCTGAGAACGGGCAACTTTACCTTCAGCTACACCTTTGAGGAAGTGCCTTTCCAC 1266	661 AGCAGCTACGCGCACAGAGCCTGGACCGGCTGATGAATCCTCTCATCGACCAATAC 720 	721 CTGTATTACCTGAACAGAACTCAAAATCAGTCCGGAAGTGCCCAAAACAAGACTTGCTG 780 	781 TITAGCGIGGGTCTCCAGCTGCCIGTCAGCCCAAAAACTGGCTACCTGGACCC 840 	841 IGITATCGGCAGCAGCGCGTTTCTAAAACAAAACAGACAACAACAACAACAACAACAACATTTACC 900 	901 TGGACTGGTGCTTCAAATATAACCTCAATGGGCGTGAATCCATCATCAACCCTGGCACT 960 	961 GCTATGGCCTCACACAAGACGACGAAGACTACTTTCCCATGAGCGGTGTCATGATT 1020 	1021 TTTGGAAAAGAGGGCCGGAGCTTCAAACACTGCATTGGACAATGTCATGATTACAGAC 1080 	1081 GAAGAGAAATTAAAGCCACTAACCCTGTGGCCACCGAAAGATTTGGGACCGTGGCAGTC 1140 	1141 AATTICCAGAGCACACACACCCTGCGACCGGAGAIGIGCGATGCTATGGGAGCATTA 1200 	1201 CCTGGCATGGTGGCAAGATAGAGACGTGTACCTGCAGGGTCCCATTTGGGCCAAAATT 1260 	1261 CCTCACACAGAIGGACACTTTCACCCGTCTCCTCTTATGGGCGGCTTTGGACTCAAGAAC 1320 	1321 CCGCCTCCTCAGATCCTCATCAAAAACACGCCTGTTCCTGCGAATCCTCCGGCGGAGTTT 1380 	1381 TCAGCTACAAAGTTTGGTTCATTCATCACCCAATACTCCACAGGACAAGTGAGTG
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November 28, 2005, 18:24:29 ; Search time 7013:94 Seconds (without alignments) 14735.325 Million cell updates/sec
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		DOG92248 BOYGEN 20573 normal cattl RZPDP1056M0360Q 5', mRNA C0892248.1 GI:51822548 EST. BOS taurus (cow) BOS taurus (cow) BOS taurus, Metazoa; Chord Mammalia; Butheria; Laura Pecora; Bovidae; Bovinae; I (bases 1 to 2.64) Hennig,S., Janitz,M., Herr Generation, annotation, eintegration of 14969 catt Unpublished (2004) Contact: Hennig S Haboraty 123, dept.Lehrac Max-Planck-Institut fuer Innestr. 63-73, D-14195 Be Fax: +49 30 8413 180 Email: hennig@molgen.mpg. Fex: +49 30 8413 180 Email: hennig@molgen.mpg. CONFP 1 to reduce sequenci procedure, clones that di battery of 200 8mer oligo clone per ONFP cluster wa filters are distributed v Genomforschung GmbH (http PCR PRIMERS FORWARD: S' CCCCAGGCTTTAC BACKWARD: S' CCCCAGGCTTTAC ACGING LOGALIST ACGING LAST AC
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/mol_type="genomic DNA"
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laboraty 123, dept.Lehrach
Max-Planck-Institut fuer Molekulare Genetik
Max-Planck-Institut fuer Molekulare Genetik
Innestr.63-73, D-14195 Berlin, Germany
Tel: +49 30 8413 13612
Fax: +49 30 8413 1360
Email: hennig@molgen.mpg.de
Email: hennig@molgen.mpg.de
The library was characterised by oligonucleotide fingerprinting
Tooredure, clones that display the same hybridiastion matrix with a
procedure, clones that display the same hybridiastion matrix with a
battery of 200 8mer oligonucleotides are grouped into clusters. One
clone per ONFP cluster was selected for sequencing. cDNA clones and
filters are distributed via Deutsches Ressourcenzentrum fuer
Genomiconschung GmbH (http://www.rzpd.de).
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(Chases 1 to 195)
Hennig, S., Janitz, M., Herwig, R. and Williams, J.

(Chases of the contraint of
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/clone_lib="normal cattle brain"
/note="Organ: brain; Vector: pSport1; Site_1: Not1;
Site_2: Sal1; Random primed and directionally cloned in
pSport1 vector using Not1
(5,-pGACTACTTCTAGATCGCGAGCGCCCC (T)15-3' and Sal1 5'-
TCGACCCACGCGTCCG-3' adapters (Gibco BRL)"
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Seq primer: 5'-CCGGTCCGGAATTCCCGGGT-3' (M13FSP).
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/mol_type="mRNA"
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Eukaryotta; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Rodentia; Sciurognathi; Murcidea; Muridae; Murinae; Rodentia; Sciurognathi; Murcidea; Murinae; Mus. Sciurognathi; Murcidea; Murinae; Mus. 1 (bases 1 to 753)

2 Lao, S., Nierman, W., Malek, J., Shatsman, S., Akinret, B., Levins, M., Russell, D., de Jong, P. and Fraser, C.M.

Russell, D., de Jong, P. and Fraser, C.M.

Mouse BAC End Sequences from Library RPCI-24

Unpublished (1999)

Ocher 268s: RECI-24-358F16.TJ

Contact: Shaying Zhao

Department of Eukaryotic Genomics

The Institute for Genomic Research

9712 Medical Center Dr., Rockville, MD 20850, USA

Tel: 301 838 0200

Fax: 301 838 0200

Fax: 301 838 0200

Rail: szhaodetigr.org

Clones are derived from the mouse BAC library RPCI-24. For BAC library availability, please contact Pieter de Jong

(pdejong@mail.cho.rg) Clones may be purchased from BACPAC Resources (http://www.chori.org/bacpac/orderingframe.htm). BAC end page: http://www.tigr.org/tdb/bac_ends/mouse/bac_end_intro.html

Plate: 358 row: F column: 16

Seq primer: T7

Class: BAC ends
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                                                                                      /tissue_type="brain tissue"
/dev stage="adult brain"
/clone_lib="normal cattle brain"
/note="Organ: brain; Vector: pSportl; Site_1: Not1;
Site_2: Sal1; Random primed and directionally cloned in
sportl vector using Not!
(5'-pAACTAGTTCAGAGGGGGGCGCCC (T)15-3' and Sal1 5'-
TCGACCCAGGGTCCG-3' adapters (Gibco BRL)"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     194 chgracrccacadacadgrcadcardadarcadrcangradgadrracadaaadraanaraacadc
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           2077 AAGCGCTGGAATCCCGAAGTGCAGTACACATCCAATTATGCAAAATCTGCCAACGTTGAT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   2017 CAATACTCCACAGGACAAGTGAGTGTGGAAATTGAATGGGAGCTGCAGAAAAAACAGC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   134 AAACGGTGGAATTCCGAAATTCAGTACACTTCCAACTACAACAAGTCTGTTAATGTGGAT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ö
                                                                                                                                                                                                                                                                                                                                                                                                                        Length 195;
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RPCI-24-158F16.TV RPCI-24 Mus musculus genomic clone
RPCI-24-158F16, genomic survey sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    42; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match 5.7%; Score 125.8; DB 7; Best Local Similarity 78.2%; Pred. No. 4.9e-24; Matches 151; Conservative 0; Mismatches 42;
/db_xref="taxon:9913"
/clone="RZPDp1056009600"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Location/Qualifiers
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          BH115587.1 GI:14954954
                                                                  /sex="female
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ACCCGTCCCCTGT 2209
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                N
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EST 13-MAR-2002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     332
                                                                                                                                                                 Email: szhao@tigr.org
Clones are derived from the rat BAC library CHORI-230
Clones are derived from the rat BAC library CHORI-230
(http://www.chori.org/bacpac/rat230.htm). For BAC library
availability, please contact Fieter de Jong (pdejong@mail.cho.org).
Clones may be purchased from BACPAC Resources
(http://www.chori.org/bacpac/or ering_information.htm). BAC end
page: http://www.tigr.org/tdb/bac_ends/rat/bac_end_intro.html
Plate: 375 row: A column: 22
Seg primer: SP6
Class: BAC ends.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CAACCTCGGGCGAGCAGTCTTCCAGGCCAAAAGCGGGTTCTCGAACCTCTCGGTCTGGT 395
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   304 gracagciccrergegaagcagaaarrcaagaaaarccaaacagargcrirrrccagagg 363
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              364 CAATCTCAACCAAGTACTCTTCCAGGCTAAAAAGAGACTTCTGGATCCCTTTGACCTGGT 423
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     BJ432209 367 bp mRNA linear EST 13-MAR-20
BJ432209 Dictyostelium discoideum cDNA library, VF Dictyostelium
discoideum cDNA clone ddv18d02 3', mRNA sequence.
BJ432209
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /cell_type="Brain"
/clone_lib="CHORI-230 Segment 2"
/noce="Vector: pTARBAC1.3; Site_1: Mbo1; Site_2: Mbo1;
CHORI-230 Rat (BN/SBNH6d/MCW) BAC library produced by
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Eukaryota, Mycetozoa, Dictyostellida, Dictyostelium.
1 (bases 1 to 367)
Urushihara, H., Tanaka, Y., Kohara, Y. and Shin-i, T.
Full length cDNA of Dictyostelium discoideum at the vegetative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     GTATAACCACGCCGACGCCGAGTTTCAGGAGCGTCTGCAAGAGATACGTCTTTTGGGGG
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                                                                                                     USA
                                                                                                  MD 20850,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Contact: Tadasu Shin-i
Center For Genetic Resource Information
National Institute of Genetics
National Institute of Genetics
Tel: Mishima, Shizuoka 411-8540, Japan
Tel: 81-559-81-6856
Fax: 81-559-81-6855
Email: tshini@genes.nig.ac.jp.
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /organism="Rattus norvegicus"
/mol_type="genomic DNA"
/strain="BN/SsNHsd/MCW"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match 2.3%; Score 50.6; DB Best Local Similarity 60.6%; Pred. No. 0.02; Matches 83; Conservative 0; Mismatches
Other GSSs: CH210-375A22.TV
Contact: Shaying Zhao
Department of Eukaryotic Genomics
The Institute for Genomic Research
9712 Medical Center Dr., Rockville, MD
Tel: 301 838 0208
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /db xref="taxon:10116"
/clone="CH230-375A22"
                                                                                                                                                                                                                                                                                                                                                                                                                      Location/Qualifiers
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Dictyostelium discoideum
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Pieter de Jong"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /sex="Female"
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BJ432209/c
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KEYWORDS
SOURCE
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                                                                                          /cell_type="Spleen/Brain"
/clone_lib="RPCI-24"
/note="Vector: pTARBAC1; Site_1: BamH1; Site_2: BamH1;
/note="Wector: pTARBAC1; Site_1: DamH1; Site_2: BamH1;
/note="Vector: produced by Pieter de Jong. The library was cloned in the pTARBAC1 cloning vector at the BamH1 sites using MboI partially digested male C57BL/6J DNA."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 685
                                                                                                                                                                                                                                                                                                                                                                                                                           CGTACCTGCGGTATAACCACGCCGACGCCGAGTTTCAGGAGCGTCTGCAAGAAGATACGT 325
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CTTGTCTCCAATAAAATCACACAGAAGCAGAGTTTCAGGAGAAAACTCCAAGTACAATAC 266
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CTTTTGGGGGCAACCTCGGGCGAGCAGTCTTCCAGGCCAAGAGCGGGTTCTCGAACCTC 385
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         267 TTTTTTTGGCA-----GGAACCGTGCCAATGCCAAAGAAAAGGGTTCTCAAACCCA 318
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         363
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    446 CGCCACAGAGCCAGACTCCTCGGGCATCGGCAAGACAGGCCAGCAGCCCGCTAAAA 505
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ----AGATTCGACCTTAAACTCCTCCCCACATGAAGGAAGTACACTCGCTCTTTTCAGA 419
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    GTTATGCCAAAAACAGTAGAAGTGGAGGCTGGCTCATTAGTCTATGACAACAGATGTA 479
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 GAGAACCTCCAGCAACCCCCGGCTGCTGGGACCTACTACAATGGCTTCAGGCGGTGGCG 625
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               480 GCAGTTTCCAGCAGATATCCTCCAATTTAGACACTTCTÁTAATCTCTGGAGCTGGAGGTC 539
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               540 TACTAATGGGCAACAACAAC-CAGACACTGATGGAGTGAGCAATGCCATGGATGATTGGC 598
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Rattus norvegicus
Rattus norvegicus
Bukaryota: Metaczos, Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Buarchontogilres; Glires; Rodentia;
Sciurognathi; Muroidea; Muridae; Murinae; Rattus.
1 (bases 1 to 803)
2 hao, 8., Shetty, J., Shatsman, S., Tsegaye, G., Geer, K.,
Shvartsbeyn, A., Gebregeorgis, E., Overton, L., Russell, D., Chen, D.,
Rat BAC End Sequences from Library CHORI-230 MboI segment
Unpublished (1999)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CACCAATGGCAGACAATAACGAAGGCGCCGACGGAGGGGGTAATGCCTCAGGAAATTGGC
                                                                                                                                                                                                                                                                                                                                                                           Gaps
                                                                                                                                                                                                                                                                                                                                                                           28;
                                                                                                                                                                                                                                                                                                                         Length 753;
                                                                                                                                                                                                                                                                                                                      Score 76.2; DB 9; Length 7
Pred. No. 1e-09;
0; Mismatches 223; Indels
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CH230-375A22.TJ CHORI-230 Segment 2 Rattus
CH230-375A22, genomic survey sequence.
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                              /db_xref="taxon:10090"
/clone="RPCI-24-358F16"
          /strain="C57BL/6J"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        BZ265284.1 GI:23978528
                                                                                                                                                                                                                                                                                                                         3.4%;
nilarity 51.6%;
Conservative (
                                                                                /sex="Male"
                                                                                                                                                                                                                                                                                                                         Query Match
Best Local Similarity
Matches 268; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    746
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AUTHORS
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Web: www.genoscope.cns.fr)
This sequence is a single read and was generated as part of a large scale clone-end sequencing project of the Terraodon nigroviridis genome. For more information, please take a look at http://www.genoscope.cns.fr/Tetraodon.
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CNS02EOD 681 bp DNA linear GSS 01-SEP-2000 letracdon nigroviridis genome survey sequence T7 end of clone 262H14 of library G from Tetracdon nigroviridis, genomic survey
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Submitted (12-APR-2000) Genoscope - Centre National de Sequencage
BP 191 91006 EVRY cedex - FRANCE (B-mail : segref@genoscope.cns.fr
                                                                                                                                                                                                          ACAACCACTACTTCGGCTACAGCACCCCTGGGGGTATTTTGATTTCAACAGATTCCACT 868
                                                                                                                                                                                                                                                                                                                  268 ACAACAGCATCATCAACAACAACACCATCACCAACAACAGGACAACAACAACAGCACCAACA 327
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           929 AGAGACTCCAACTTCAAACTCTTCAACATCCAAGTCAAGGAGGTCACGAAGAAGATGATGGCG 988
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               388 ACAACAGGAACAACAACAGCACCAACAGGAACAAGACAGCAACACACAGAAATACATCAATA 447
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            GSS; genome Burvey Requence.

Tetracdon nigroviridis
Tetracdon nigroviridis
Eukaryota, Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Eukaryota, Metazoa; Chordata; Craniata; Vertebrata; Buteleostemi;
Actinopterygii; Neoperygii; Percomorpha; Tetracodontiformes;
Tetracontoides; Tetracodontidae; Tetracodon.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Roest Crollius, H., Jaillon, O., Dasilva, C., Bouneau, L., Fisher, C., Bernot, A., Fizames, C., Wincker, P., Brottier, P., Quetier, F., Sauxin, W. and Weissenbach, J.

Estimate of human gene number provided by genome-wide analysis using Tetraodon nigroviridis DNA sequence

Nat. Genet. 25 (2), 235-238 (2000)
                                                                                                     148 GCAACTACAGAAGCACCAACAACATCATCAACAACAACAACAGCGGGGAACAACAACA
                                                                                                                                                           CCACCTACAATAACCACCTCTACAAGCAAATCTCCAGTGCTTCAACGGGGCCAGCAACG
                                                                                                                                                                                                                                                                                                                                                                                                            GCCACTTTTCACCACGTGACTGGCAGCGACTCATCAACAACAATTGGGGATTCCGGCCCA
                                                   GCGATTCCACATGGCTGGGCGACAGAGTCATCACCACCAGCACCCGCACCTGGGCCTTGC
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     Gape
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0; Mismatches 190; Indels

    .681
    .6xganism="Tetraodon nigroviridis"
/mol_type="genomic DNA"
/db_xref="taxon:99883"

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AL193990.1 GI:7832096
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Pularayota, Metazoa, Chordata, Urochordata, Ascidiacea, Enterogona,

Phlebobranchia, Clonidae, Ciona.

1 (bases 1 to 581)

Satou, Y., Shin-I,T., Kohara,Y. and Satoh,N.

Expressed genes in Ciona intestinalis (2004)
                                                                                                                                                                                                                                                                                                                                                                                               716 TCATCACCACCACCACCACCTGGGCCTTGCCCACCTACAATAACCACCTCTACAAGC 775
                                                                                                                                                                                                                                                                                                                                                                                                                                                328 TCAACAACATCANCAACATCAANTACCTCTAAACCAACAACTACATCAACATCAACT 269
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       776 AAATCTCCAGTGCTTCAACGGGGCCAGCAACGACCACTACTTCGGCTACAGCACCC 835
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     268 ACATCAACTACCTCTAAACCAACAACCACATCAACTACATCAACTACATCAACTACATCA 209
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          208 actactrocaaaccaactactacatcaccaccactaactactrocaaaacaactactact
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         836 CCTGGGGGTATTTTGATTTCAACAGATTCCACTGCCACTTTTCACCACGTGACTGGCAGC 895
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/mol type="mRNA"
/do rate="taxon:719"
/close="cidgs1fis"
/tissue_type="digestive gland"
/dev_stage="adult"
/clone_lib="Yuteaka Satou unpublished cDNA library, adult digestive gland"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       148 TCATCAACAACAACAACTGGTTCATCAACAACAACTGGTTCATCAACAACCACATCATCA 89
                                                                                                                                                                                    /dev_stage="Growth phase"
/clone_lib="Dictyostelium discoideum cDNA library, VF"
                                                                                                                                                                                                                                                                                                                                           Gaps
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                                                                                                                                                                                                                                                                                       Query Match 2.2%; Score 48; DB 3; Length 367; Best Local Similarity 49.6%; Pred. No. 0.085; Matches 120; Conservative 0; Mismatches 122; Indels
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                     /organism="Dictyostelium discoideum"
/mol_type="mRNA"
/strain="AX4"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Kyoto University
Sakyo-ku, Kyoto, Kyoto 606-8502, Japan
Tel: 81-75-753-4055
Fax: 81-75-705-1113
Email: yucaka@acidian.zool.kyoto-u.ac.jp.
Location/Qualifiers
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                                                                                                  /db_xref="taxon:44689"
/clone="ddv18d02"
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Department of Zoology
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Best Local Similarity
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VERSION KEYWORDS SOURCE ORGANISM

REFERENCE AUTHORS TITLE JOURNAL COMMENT

FEATURES

DEFINITION

RESULT 6 BW335572

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Triticum aestivum (bread wheat)
Triticum aestivum
Triticum aestivum
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Pooideae; Triticeae; Triticum.
El (bases 1 to 581)
Sido, K., Bai, G. H. and Carver, B.F.
Nylon Filter Arrays Reveal Differential Expression of Expressed
Sequence Taga in Wheat Roots Under Aluminum Stress
L J. Integr. Plant Biol. 47 (7), 839-848 (2005)
Contact: Guihua Bai
USDA/ARS and Department of Agronomy
Kansas State University
Manhattan, KS 66506, USA
Email: gbai@bear.agron.ksu.edu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CF569196 581 bp mRNA linear EST 08-SEP-2004 EST057 Subtracted, Clontech (cat. # K1804-1) Triticum aestivum cDNA clone FDC57 5', mRNA sequence.
                871 CACTITICACCACGIGACIGGCAGCGACICATCAACAACAAITGGGGAITCCGGCCCCAAG 930
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   931 AGACTCCAACTTCAAACTCTTCAACATCCAAGTCAAGGGGGTCACGACGAATGATGGCGTC 990
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /tissue type="root"
/clone Tib="Subtracted, Clontech (cat. # K1804-1)"
/note="EST from wheat (Triticum aestivum, cv. OK91G106)
                                                                                                                                                                                                                                                                                                                                           751 ACCTACAATAACCACCTCTACAAGCAAATCTCCCAGTGCTTCAACGGGGGCCCAGCAACGAC
                                                                                                                                                                                                                                                                                                                                                                                                                      811 AACCACTACTTCGGCTACAGCACCCCTGGGGGTATTTTGATTTCAACAGATTCCACTGC
                                                                                                                                                                                                                                                                                                                                                                                                                                                              Length 869;
                                                                                                                                                                                                                                                                                                    0; Mismatches 139; Indels
                                                                                                                                                                                                                                                          2.1%; Score 45.6; DB 7;
48.1%; Pred. No. 0.56;
cultivar="Wheat line PI 178383"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            518
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High quality sequence stop: 581.
Location/Qualifiers
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/clone="FDC57"
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/cultivar="OK91G106"
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Matches 129;
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This sequence is the direct result of the Base calling software
Phred (default parameters). It is the raw base calls. To aid in the
identification of the high quality insert the software Lucy
(default parameters) has been run on this sequence. Lucy identified
the region [128,636].
Plate: Talt537 row: N column: 23.
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Genswein, B., Graf, R., Gulick, P., Hrycan, L.D., Laroche, A.,
Links, M.G., McGarthy, B.L., Monroy, A., Muzak, I., Nilson, D.,
Penniket, C., Roach, J.L. and Sarhan, F.
Functional Genomics of Abiotic Stress In Wheat and Canola Crops
Unpublished (2003)
Contact: Wm L Crosby
                                                                                                                                                                                                                                           GACAACAACGACGACRACGACGACAACAAAAACGACRACGGCGACGACGACGACGACAAC 292
                                                                                                                                                                                                                                                                                   697 ACATGGCTGGGCGACAGAGTCATCACCACCAGCACCGGCACCTGGGCCTTGCCCACCTAC 756
                                                                                                                                                                                                                                                                                                                                                                                                                                             817 TACTTCGGCTACAGCACCCCCTGGGGGTATTTTGATTTCAACAGATTCCACTGCCACTTT 876
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     877 TCACCACGTGACTGGCAGCGACTCATCAACAATTGGGGGATTCCGGCCCAAGAGACTC 936
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1 (bases 1 to 869)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    mRNA linear EST 05-DEC-2 Talt5 Triticum aestivum cDNA,
                                                                                                                                                                                                    GACAATAACGAAGGCGCCGACGGAGTGGGTAATGCCTCAGGAAATTGGCATTGCGATTCC
                                                                                                                                                                                                                                                                                                                         RACGGCAGCGACGACGACGACGACAACAAAAACRGCAACRACGACGGCGACRACAAC
                                                                                                                                                                                                                                                                                                                                                                757 AATAACCACCTCTACAAGCAAATCTCCAGTGCTTCAACGGGGGCCAGCAACGACGACCAC
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                                                                                                                                                                ;
                      /clone lib="G"
/note="Genoscope sequence ID : COAG262DD07LP1
end : T7"
                                                                                                                         Length 681;
                                                                                                                                                              Indels
                                                                                                                    ; Score 45.6; DB 10;
; Pred. No. 0.51;
10; Mismatches 178;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            937 AACTICAAACTCTICAACATCCAAGGA 968
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              organism="Triticum aestivum"
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    /clone="262H14"
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                                                                                                                      Query Match 2.1%;
Best Local Similarity 43.4%;
Matches 144; Conservative 1
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CM931784 1075 bp DNA linear GSS 24-FEB-2005
EDCC981TF A. castellanii, 6-8 kb library from total genomic DNA
Acanthamoeba castellanii genomic clone EDCC981, genomic survey
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Bukaryota; Acanthamoebidae; Acanthamoeba.

I (bases 1 to 1075)
Anderson, I.J. and Loftus, B.J.
Gene discovery in the Acanthamoeba castellanii genome
Unpublished (2004)
Contact: Iain Anderson
The Institute for Genomic Research (TIGR; www.tigr.org)
9712 Medical Center Drive, Rockville, MD 20850, USA
Tel: 301-795-798
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  141 GCCAGGCCAGGGCCAGGGCCAGGGCCAGGACCAGGCCAGGACCAGAC
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                                                                                    /mol type="genomic DNA"
/db xref="taxon:99883"
/clone="129H24"
/clone lib="Genoscope sequence ID : COBG129DD12LP1
end : T7"
                                                                                                                                                                                                                                                                                                                                                                 Length 983;
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/mol_type="qenomic DNA"
/strain="Neff"
                                     l. .983
/organism="Tetraodon nigroviridis"
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Best Local Similarity 54.1%; Pred. No. 0.78;
Matches 92; Conservative 0; Mismatches 78;
                                                                                                                                                                                                                                                                                                                                                          Score 45.4; DB 11;
Pred. No. 0.66;
0; Mismatches 156;
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/clone="EDCC981"
/clone_lib="A. castellan11,
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illarity 47.1%;
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Direct Submission

Direct Submission

By 191 91006 EVRY cedex - FRANCE (E-mail : seqref@genoscope.cns.fr

Web : www.genoscope.cns.fr)

This sequence is a single read and was generated as part of a large scale clone-end sequencing project of the Terracdon nigroviridis genome. For more information, please take a look at http://www.genoscope.cns.fr/Tetracdon.
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Tetraodon nigroviridis genome survey sequence T7 end of clone
129H24 of llbrary G from Tetraodon nigroviridis, genomic survey
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sctinopteryygii; Veopterygii; Teleostei; Buteleostei; Neoteleostei;
Acanthomorpha; Acanthopterygii; Percomorpha; Tetraodontiformes;
Tetradontoidea; Tetraodontidae; Tetraodon.
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                                                                                                                                                                    Gaps
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                                                                                                    Length 581;
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      root in response to aluminum stress"
                                                                                                 Query Match
2.1%; Score 45.4; DB 6;
Best Local Similarity 46.6%; Pred. No. 0.55;
Matches 145; Conservative 0; Mismatches 166;
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AL302828.1 GI:8183374
GSS; genome survey sequence.
Tetraodon nigroviridis
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/ Organism="Mono Saptens"
/ for it yes="mRNA"
/ wol type="mRNA"
/ db_xref="taxon:9606"
/ clone="INAGE:272826"
/ lab hose="MRNA"
/ clone="INAGE:272826"
/ lab hose="Dation (life Technologies)"
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Contact: Robert Strausberg, Ph.D.
Contact: Capbbs-rémail.nih.gov
Oligo-dr track not found, Not I site shown in beginning of sequence
is likely internal to the message. cDNA Library Preparation: M.B.
Soares Lab Clone distribution: NCI-CGAP clone distribution
information can be found through the I.M.A.G.E. Consortium/LLNL at:
www-bio.llnl.gov/bbrp/image/image.html
                                                                                                                                                                                                                                                                                                                                                                                                                                           322 bp mRNA linear EST 02-DEC-1999
UI-H-BII-afs-a-02-0-UI.s1 NCI_CGAP_Sub3 Homo sapiens cDNA clone
IMAGE:2722826 3', mRNA sequence.
                                                208 rererggeriaceacidecageraciaedecececidaaggggregaggeregageecererg 149
                                                                                                                                                                         148 AGCTCACCCAGTCTGACCCACGACGAGGGGCTCCCCAAGCACCTGGAAGAGCTCGACAAG 89
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Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Hominidae, Homo.
1 (bases 1 to 322)
NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
                                                                                                                     205 GACGCAGCGCCCTCGAGCACACGACAAGGCCTACCGACCAGCAGCTCAAAGCGGGTGACAAT
145 GGCTACAAGTACCTCGGACCCTTCAACGGACTCGACAAGGGGGGGCCCGTCAACGCGGCG
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AW206887.1 GI:6506383
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Unpublished (1997)
                                                                                                                                                                                                                                                    265 CCGTACCTG 273
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AW206887/c
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/clone lib="NOI CGAP Kid11"
/clone lib="NOI CGAP Kid11"
/clone lib="NOI CGAP Kid11"
/note="Grgan: Kidney; Vector: pT7T3D-Pac (Pharmacia) with a modified polylinker; Site 1: Not 1; Site 2: Ecc RI; Plasmid DNA from the normalTzed library NOI CGAP Kid3 was prepared, and se circles were made in vitro. Following HAP purification, this DNA was used as tracer in a subtractive hybridization reaction. The driver was PCR-amplified cDNAs from a pool of 5,000 clones made from the same library (clonesIDS 132276-1323911, 1456007-1456775, and 1500552-1502855). Subtraction by Bento Soares and M. Fatima Bonaldo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Email: cgapbs-remail.nih.gov.

Email: cgapbs-remail.nih.gov.

Emmert-Buck, M.D., Ph.D.

CDNA Library Preparation: M. Bento Soares, Ph.D.

CDNA Library Arrayed by: Greg Lennon, Ph.D.

CNA Library Arrayed by: Greg Lennon, Ph.D.

CNA Sequencing by: Washington University Genome Sequencing Center

Clone distribution: NCI-CGAP clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:

Www-blo.llnl.gov/bbrp/image/image.html

Insert Length: 326 Std Error: 0.00

Seq primer: -40UP from Gibco.
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289 bp mRNA linear EST 20-DEC-1999 wh46h04.x1 NCI CGAP Kidl1 Homo sapiens cDNA clone IMAGE:2383831 3' similar to TR:000613 000613 T3 RECEPTOR-ASSOCIATING COFACTOR-1. [1] ', mRNA sequence.
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                                                                                                                                                            219
                                                                                                                                                                                                                       Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
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1 (bases 1 to 289)
NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
                                       GCCAACCAGCAAAAGCAGGACGACGGCCGGGGTCTGGTGCTTCCTGGCTACAAGTACCTC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              160 GGACCCTTCAACGGACTCGACAAGGGGGAGCCCGTCAACGCGGGGGGACGCAGGGGCCCTC
                                                                                                                                                                                                                                                                                                                                                      578 GACCTGGTCAAGGAGTACGAGAAGGAGAAGCAGCGCGCGACGACCTGGA 529
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Contact: Robert Strausberg, Ph.D.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /organism="Homo sapiens"
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/db_xref="taxon:9606"
/clone="IMAGE:2383831"
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Contact: Robert Strausberg, Ph.D.
Email: cgapbs-remail.nih.gov
Tissue Procurement: Ash Alizadeh, John Byrd, M.D., Mike Grever,
Tissue Procurement: Ash Alizadeh, John Byrd, M.D., Mike Grever,
M.D., Louis M. Staudt, M.D., Ph.D.
CDNA Library Preparation: M. Bento Soares, Ph.D.
CDNA Library Arrayed by: Greg Lennon, Ph.D.
DNA Sequencing by: Mashington University Genome Sequencing Center
Clone distribution: NCI-CGAP Clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
www-bio.llnl.gov/bbrp/image/image.html
Insert Length: 63 Std Brror: 0.00
Seq primer: -40UP from Gibco
High quality sequence stop: 438.
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                                                                                                                                                                                                                            145 GGCTACAAGTACCTCGGACCCTTCAACGGACTCGACAAGGGGGAGCCCCGTCAACGCGGCG 204
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       Average insert size 1.3 kb. Library enriched for full-length clones and constructed by Life Technologies. Note: this is a NIH_MGC Library."
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Mammalia; Butheria; Buarchontoglires; Primates; Catarrhini;
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1 (bases 1 to 451)

NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.

NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.

Tutional Cancer Institute, Cancer Genome Anatomy Project (CGAP),

Tumor Gene Index

Unpublished (1997)
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                                                                                                                              DB 2; Length 356;
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Best Local Similarity 52.4%; Pred. No. 0.6;
An Conservative 0; Mismatches
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A1439550.1 GI:4305107
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1475592-1476743); NCI CGAP Pr22 pool 1 LLAM 2457-2459, 2758-2759, 3062-3068 [IMAGE CloneIDS 985608-986759, 1101192-1101959, 127928-1220615); NCI CGAP COLO pool 1 LLAM 244-2653, 2871-2872 (IMAGE CloneIDS 1057446-1061255, 1144584-1145351), Subtraction was performed as previously and Subtraction: Two Approaches 10996; Normalization and Subtraction: Two Approaches To Facilitate Gene Discovery. Genome Research 6, 791-806.

TAG ILSB-NCI CGAP_LUS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         BG170384 1356 bp mRNA linear EST 06-FEB-2001 602322706F1 NIH_MGC_89 Homo sapiens cDNA clone IMAGE:4426104 5',
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/db xref="taxon.9606"
/clone="IMAGE:445104"
/lab_host="hypernephroma, cell line"
/lab_host="hypernephroma, cell line"
/lab_host="hypernephroma, cell line"
/clone lib="hypernephroma, dapters
/clone lib="nimage" dapters
/note="lorgan: kidney, vector: pGMV-SPORT6; Site 1: Not1;
site_2: Sall; Cloned unidirectionally; oligo-dT_primed.
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Email: cgapbs-remail.nth.gov
Tissue Procurement: ATCC
CDNA Library Preparation: Life Technologies, Inc.
CDNA Library Arrayed by: The I.M.AG.B. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can
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0
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http://image.llnl.gov
Plate: LLnM1012 row: k column: 01
High quality sequence stop: 353.
Location/Qualifiers
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Homo sapiens
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RESULT 1

US-09-807-802A-12

Sequence 12, Application US/09807802A

Patent No. 6759237

GENERAL INVENTION:

APPLICANT: Xiao, Weidong

TITLE OF INVENTION: Adeno-Associated Virus Serotype I Nucleic Acid Sequences,

TITLE OF INVENTION: Adeno-Associated Virus Serotype I Nucleic Acid Sequences,

TITLE OF INVENTION: Adeno-Associated Virus Serotype I Nucleic Acid Sequences,

TITLE OF INVENTION: Adeno-Associated Virus Serotype I Nucleic Acid Sequences,

CURRENT APPLICATION NUMBER: US/09/807,802A

CURRENT FILING DATE: 1998-11-05

PRIOR PALICATION NUMBER: US 60/107,114

PRIOR PILING DATE: 1998-11-05

PRIOR APPLICATION NUMBER: US 60/107,114

PRIOR PILING DATE: 1999-11-05

NUMBER OF SEQ ID NOS: 20

SOFTHARE: PatentIn version 3.1

SEG ID NO 12

LENGTH: 2211
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US-08-647-655-2
US-09-807-802A-6
US-09-807-802A-6
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100.0%; Score 2209;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 2209; Conservative 0; Mismatches
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                       ; LOCATION: (1)..(2208)
; OTHER INFORMATION:
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  TYPE: DNA
ORGANISM: AAV-1
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100.0%; Score 2209;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 2209; Conservative 0; Mismatches
PRIOR APPLICATION NUMBER: US 60/107,114
PRIOR FILING DATE: 1999-11-05
PRIOR PELLING DATE: 1999-11-02
PRIOR FILING DATE: 1999-11-02
NUMBER OF SEQ ID NOS: 20
SEQ ID NO 1
LENGTHARE: PALENTIN version 3.1
SEQ ID NO 1
LENGTH: 4718
TYPE: DNA
ORGANISM: AAV-1
FETATURE:
NAME/KEY: CDS
LOCATION: (335)..(2206)
OTHER INFORMATION:
PETATURE:
PETATURE
                                                                                                                                                                                                                                                                          LOCATION: (2223) . (4430) ; OTHER INFORMATION: US-09-807-802A-1
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8686868686	8 8 8 8 8 8 8 8 8 8	6 8 6 8 6 8 6 8 6 8 6
Db 4023 GCATTACCTGGCATGGCAAGATAGAGACGTGTACCTGCAGGGTCCCATTTGGCC 4082 1861 AAAATTCCTCACACAGATGGCAACTTTCACCCGTCTCTTATGGGCGGCTTTGGACTC 1920 4083 AAAATTCCTCACACAGATGGACTTTCACCCGTCTCTTATGGGCGGCTTTGGACTC 1142 bb 4143 AAGAACCCGCTCCTCAGATCCTCATAAAACACGCTGTTCCTGCGAATCCTCCGGGG 1980 4143 AAGAACCCGCTCCTCAGATCCTCATCATAAAACACGCTGTTCCTGCGAATCCTCCGGGG 1202 bb 4203 GAGTTTTCAGCTACAAAGTTTGCTTCATCACCCCAATACTCCACAGGACAATCCTCGGGG 4202 09 2041 GTGGAAATTGAAAGTTTGTTCATTCATCACCCAATACTCCACAGGACAAGTGAGT 2040 bb 4203 GAGTTTTCAGCTACAAAGTTTGTTCATTCATCACCCAATACTCCCAAGGACAAGTGAGT 4262 2041 GTGGAAATTGAAAAGTTGCTAAAAGAAAAAAAAACACCAATACTCCCAAGGACAAGTGAGG 4322 205 3 GTGGAAATTGAAAAGTTGCAAAAAAAAAAAAAAAAAAAA	WESULT 1980-11 Sequence 11, Application US/10216870 Sequence 11, Application US/10216870 Patent No. 6723551 GENERAL INFORMATION: APPLICANT: WRABATION: APPLICANT: URABE, MASASHI TILLE OF INVENTION: PRODUCTION OF ADENO-ASSOCIATED VIRUS IN INSECT CELLS CURRENT APPLICATION NUMBER: US/10/216,870 CURRENT FILING DATE: 2002-08-13 NUMBER OF SEQ ID NOS: 24 SOFTWARE: Patentin version 3.1 SEQ ID NO 11 LENGTH: 7447 TYPE: DNA ORDANISM: Artificial Sequence FEATURE: PEATURE: CTHER INFORMATION: Synthetic US-10-216-870-11	Query Match 99.7%; Score 2202.6; DB 3; Length 7447; Best Local Similarity 99.8%; Pred: No. 0; Matches 2205, Conservative 0; Mismatches 4; Indels 0; Gaps 0; Qy 1

; SOFTWARE: PatentIn version 3.1 ; SEQ ID NO 19 ; LENGTH: 4683 ; TYPE: DNA ; ORGANISM: AAV-6 US-09-807-802A-19	Query Match 95.1%; Score 2101.8; DB 3; Length 4683; Best Local Similarity 97.0%; Pred. No. 0; Matches 2142; Conservative 0; Mismatches 67; Indels 0; Gaps 0;	Db 1 ATGGCTGCCGATGTTATCTTCCAGATTGGCTCGAGGACAACCTCTCTGAGGGCATTCGC 60 Db 2208 ATGGCTGCCGATGGTTATCTTCCAGATTGGCTCGAGGACACCTCTCTGAGGCATTCGG 2267	Qy 61 GAGTGGTGGACTTGAAACCTGGAGCCCCGAAGCCCAAAGCCAAAGCAAGAG 120	Oy 121 GACGGCGGGGTCTGGTGCTTCCTGGCTACAGTACCTCGGACCCTTCAACGGACTCGAC 180	OY 181 AAGGGGGAGCCCTCAACGCGGCGACCGCCGCCTCGAGCACGACAAGGCCTACGAC 240	Oy 241 CAGCAGTCTCAAAGCGGGTGACAATCCGTACCGGGTATAACCACGCCGACGCCGAGTTT 300	Oy 301 CAGGAGCGTCTGCAAGAAGATACGTCTTTTGGGGGCAACCTCGGGCGAGCAGTCTTCCAG 360	Oy 361 GCCAAGAGCGGTTCTCGAACCTCTCGGTCTGAGGAGGCGCTAAGACGGCTCCT 420	Oy 421 GGAAAGAAACCTCCGGTAGAGCACGCCACAAGAGCCAGACTCCTCCTCGGCCATCGCC 480	OY 481 AAGACAGCCAGCAGCCGCTAAAAAGAGACTCAATTTTGGTCAGACTGGCGACTCAGAG 540	OY 541 TCAGTCCCCGATCCACAACCTCTCGGAGAACCTCCAGCAACCCCGCTGCTGTGGGACCT 600	OY 601 ACTACAATGGCTTCAGGCGTGGCGCACCAATGGCAGACGAGAGGCGCCGACGGA 660	
	dy 1501 TITACCTGGACTGGTGCTTCAAATATAACCTCAATGGGGTGAATCCATCATCAACCCT 1560 Db 6121 TITACCTGGACTGGTGCTTCAAAATATAACCTCAATGGGCGTGAATCCATCATCAACCCT 6180	Oy 1561 GGCACTGCTATGGCCTCACAAGACGACGAAGACAAGTTCTTTCCCATGAGCGGTGTC 1620 Db 6181 GGCACTGCTATGGCCTCACACAAAGACGACGAAGTTCTTTCCCATGAGCGGTGTC 6240	OY 1621 ATGATITITGGAAAAGAGGCGCCGGAGCTICAAACACTGCATTGGACAATGTCATGATT 1680 	OY 1681 ACAGACGAAGGAAATTAAAGCCACTAACCCTGTGGCCACCGAAAGATTTGGGACCGTG 1740	QY 1741 GCAGTCAATTTCCAGAGCAGCAGCACACCCTGCGACCGGAGATGTGCATGCTATGGGA 1800 Db 6361 GCAGTCAATTTCCAGAGCAGCAGCACAGACCTGCGAACCGGAGATGTGCATGCTATGGGA 6420	Qy 1801 GCATTACCTGGCATGGTGTAGAAAAAGACGTGTACCTGCAGGGTCCCATTTGGGCC 1860 Db 6421 GCATTACCTGGCATGGTGTGGCAAGATAGAGACGTGTACCTGCAGGTCCCCATTTGGGCC 6480	OY 1861 AAAATTCCTCACACAGATGGACACTTTCACCCGTCTCCTTATGGGCGGCTTTGGACTC 1920	OY 1921 AAGAACCGGCCTCCTCAGATCCTCATCAAAAACACGCCTGTTCCTGCGAATCCTCCGGCG 1980	OY 1981 GAGITITCAGCTACAAAGITIGCTTCATTCATCACCCAATACTCCAGGACAAGTGAGI 2040	OY 2041 GTGGAAATTGAATGGGAGCTGCAGAAAAACAGCAAGCGCTGGAATCCCGAAGTGCAG 2100	QY 2101 TACACATCCAATTATGCAAAATCTGCCAACGTTGATTTTACTGTGGACAACAATGGACTT 2160 DD 6721 TACACATCAATTATGCAAAATCTGCCAACGTTGATTTTACTGTGGACAACAACAATGGACTT 6721 TACACATCAATTATGCAAAATCTGCCAACGTTGATTTTACTGTGGACAACAACAATGGACTT 6760	Oy 2161 TATACTGAGCCCCCATTGGCACCCGTTACCTTACCCTCGCTGT 2209	RESULT 4 US-09-807-802A-19 US-09-807-802A-19 Sequence 19, Application US/09807802A Sequence 19, Application US/09807802A Sequence 19, Application US/09807802A Settle No. 6759237 GENERAL INFORMATION: APPLICANT: Xiao, Weidong TITLE OF INVENTION: Adeno-Associated Virus Serotype I Nucleic Acid Sequences, TITLE OF INVENTION: Vectors and Host Cells Containing Same FILE REFERENCE: GNVPN.031USA CURRENT APPLICATION NUMBER: US/09/807,802A CURRENT FILING DATE: 1998-11-05 PRIOR APPLICATION NUMBER: DC/US99/25694 PRIOR APPLICATION NUMBER: PCT/US99/25694 NUMBER OF SEQ ID NOS: 20

OY 2041 GTGGAAATTGAATGGGAGCTGCAGAAACAGCAAGCGCTGGAATCCCGAAGTGCAG 2100	RESULT 5 US-09-807-802A-14 is Sequence 14, Application US/09807802A is GENERAL INFORMATION: APPLICANT: Wilson, James M. APPLICANT: Wilson, James M. APPLICANT: Wilson, James M. TITLE OF INVENTION: Adeno-Associated Virus Serotype I Nucleic Acid Sequences, TITLE OF INVENTION: Adeno-Associated Virus Serotype I Nucleic Acid Sequences, TITLE OF INVENTION: Adeno-Associated Virus Serotype I Nucleic Acid Sequences, TITLE OF INVENTION: Adeno-Associated Virus Serotype I Nucleic Acid Sequences, CURRENT FILING DATE: 1999-11-05 PRIOR PELING DATE: 1999-11-05 PRIOR PELING DATE: 1999-11-05 PRIOR PELING DATE: 1999-11-05 SOFTWARE: Patentin version 3.1 SEQ ID NO 14 LENGTH: 1800 TYPE: DATA ORGANISM: AAV-1 FEATURE: NAME/KEY: CDS LOCATION: (1)(1797) OTHER INFORMATION:		472 GGCATCGGCAGACCCGCTAAAAAGGACTCAATTTTGGTCAGACTGGC [592 181 652 241	Qy 712 AGAGTCATCACCAGCACCCGCACCTGGCCCTACAATAACCACCTACA 771 Db 301 AGAGTCATCACCAGCACCCGCACCTGGGCCTTACCACTACAATAACCACCTCTAC 360 Qy 772 AAGCAAATCTCCAGTGCTTCAACGGGGGCCAGCAACCACCACACCACCACACCACACCAC
3108 ATCAACAACAACAATGGGGGATTCCGGCCCAAGAGCTCTTCAAGCTCTTCAACATCCAA 3167 961 GTCAAGAGGGTCACGACGAATGATGGCGTCACCATCCACCTACCAGCAC 1020 3168 GTCAAGAGGTCACGACGAATGATGGCGTCACGCACCGCTTACCAGCACG 327 1021 GTTCAAGTCTTCTCGGAGTACCAGCACCACGACCACTCGCGCTCTGCGCACCAG 1080 111	1141 CTCAACAATGGCAGCCAAGCCGTAGCATCATCCTTTTACTGCCTGGAATATTTCCCT 1200	1 GGCACTGCTATGGCCTCACAAAACACAAAACACAATTCTTTCCCATGAGCGGTGTC 1 GGCACTGCTATGGCCTCACAAAACACAAAACTGAATTCTTTCCCATGAGCGGTGTC 1 GGCACTGCTATGGCCTCAACAAAACACAAAATTCTTTCCCATGAGCGTGTC 1 ATGATTTTTGGAAAAAAGAGCGCGGAGCTTCAAAACTGCATTGACAATGTCATTGATT 1 HIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIII	1 ACAGACGAAGGAAATTAAAGCCACTAACCTGTGGCCACCGAAAGATTTGGGACCGTG ACAGACGAAGGAAATCAAAGCCACTAACCCTGTGGCCACCGAAAGATTTGGGACTGTG GCAGACGAAGAGAAATCAAAGCCACTAACCCCGTGGCCCGAAAGATTTGGGACTGTG 1 GCAGTCAATTTCCAGAGCAGCAGACCTGCGACCCGGAGATGTGCTATGGGA 1		1921 AAGAACCCGCCTCCTCAGATCCTCATCAAAACGCCCTGTTCCTGCGGATCCTCCGGCG 1980

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1501 †CCAATTATGCAAAATCTGCCAACGTTGATTTTACTGTGGACAACAACAATGGACTTATACT
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                                          2047 ATTGAATGGGAGCTGCAGAAAGAAAACAGCAAGCGCTGGAATCCCGAAGTGCAGTACACA
                                                          1441 ATTGAATGGGAGCTGCAGAAAAAAAACGCAAGCGCTGGAATCCCGAAGTGCAGTACACA
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                                                                                                TCCAATTATGCAAAATCTGCCAACGTTGATTTTACTGTGGACAACAATGGACTTTATACT
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US-09-770-315-4

Sequence 4, Application US/09770315

Patent No. 6429001

GREERAL INFORMATION:

APPLICANT: Chiron Corporation

TITLE OF INVENTION: Recombinant AAV Packaging Syf;
FILE REPERENCE: 20263-501

CURRENT APPLICATION NUMBER: US/09/770,315

CURRENT APPLICATION NUMBER: US 60/178,536

PRIOR FILING DATE: 2000-01-26
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       66.0%; Score 1458.6;
79.1%; Pred. No. 0;
iive 0; Mismatches
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SOFTWARE: FastSEQ for Windows Version 3.0
SEQ ID NO 4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                OTHER INFORMATION: recombinant DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Best Local Similarity 79.1
Matches 1747; Conservative
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ORGANISM: Unknown
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                                                   APPLICANT: Chiron Corporation
TILE OF INVENTION: Recombinant AAV Packaging Systems
FILE REFERENCE: 20263-501
CURRENT APPLICATION NUMBER: US/09/770,315
CURRENT FILING DATE: 2001-01-26
PRIOR APPLICATION NUMBER: US 60/178,536
PRIOR PILING DATE: 2000-01-26
NUMBER OF SEQ ID NOS: 8
SOFTWARE: FastSEQ for Windows Version 3.0
LENGTH: 7557
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Pred. No. 0;
0; Mismatches 459;
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           Sequence 3, Application US/09770315
Patent No. 6429001
GENERAL INFORMATION:
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                                   2503 CAGGAGCGCCTTAAAGAAGATACGTCTTTTGGGGGCAACCTCGGACGAGGAGGAGGTCTTCCAG
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                                              AAAATTCCTCACACAGATGGACACTTTCACCCGTCTCCTTATGGGCGGCTTTGGACTC
                                                                  4088 AAGATTCCACACACAGGACGGACGATTTCACCCCTCTCCCCTCATGGGTGGATTCGGACTT
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APPLICANT: Chiron Corporation
ITILE OF INVENTION: Recombinant AAV Packaging Systems
FILE REFERENCE: 20263-501
CURRENT APPLICATION NUMBER: US/09/770,315
CURRENT PILING DATE: 2001-01-26
PRIOR APPLICATION NUMBER: US 60/178,536
PRIOR APPLICATION NUMBER: US 60/178,536
NUMBER OF SEQ ID NOS: 8
SOFTWARE: FastSEQ for Windows Version 3.0
SEQ ID NO 2
LENGTH: 8698
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US-09-770-315-2
; Sequence 2, Application US/09770315
; Patent No. 642901
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ORGANISM: Unknown
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US-09-770-315-2
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                                                                                                                                                           DB 3;
                                                                                                                                                         Score 1453.6; Pred. No. 0; Mismatches
EARLIER FILING DATE: 1999-03-10
NUMBER OF SEQ ID NOS: 59
SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 5
LENGTH: 8179
                                                                                                                                                         Query Match
Best Local Similarity 79.2%;
Matches 1752; Conservative
                                                                                       TYPE: DNA ORGANISM: Virus
                                                                                                                          US-09-438-268-5
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Patent No. 6491907.

GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: Samulaki, Richard J
APPLICANT: 1999-11-10
EARLIER PILING DATE: 1999-11-10
EARLIER PILING DATE: 1999-11-10
EARLIER APPLICATION NUMBER: 60/123,651
                                                                                                3700 TACTCGTGGACTGGAGCTACCAAGTACCACCTCAATGGCAGAGACTCTCTGGTGAATCCG
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                             TTTACCTGGACTGGTGCTTCAAAATATAAACCTCAATGGGCGTGAATCCATCAACCCT
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4110 ACCACCTTCAGTGCGGCAAAGTTTGCTTCCTTCATCACACAGTCCTCCAGGGACAGGTC
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Patent No. 5658785
GENERAL INFORMATION:
GENERAL INFORMATION:
TITLE OF INVENTION: Adeno-Associated Virus Materials
TITLE OF INVENTION: Methods
NUMBER OF SEQUENCES: 3
CORRESPONDENCE ADDRESS:
ADDRESSE: MATSHALL, O'TOOLE, GETSTEIN, Murray & Boggnerer
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COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
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Pred. No. 0;
0; Mismatches
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S. Wacker
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CLASSIFICATION: 435
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: No. 5689785and, Greta B.
REGISTRATION NUMBER: 35,302
REPREMENCE/DOCKET NUMBER: 31975
TELEPHONE: (312) 474-6300
TELEPAT: (312) 474-6448
TELEPAT: 25-3866
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 4680 base pairs
TYPE: nucleic acid
TYPE: nucleic acid
TYPE: nucleic acid
TYPE: nucleic acid
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MOLECULE TYPE: DNA (genomic)
US-08-254-358-1
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Best Local Similarity 78.7%;
Matches 1740; Conservative
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COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
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STATE: Illinois
COUNTRY: USA
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                              3030 ATCAACAACAACTGGGGATTCCGACCCAAGAGACTCAACTTCAAGTTTTAACATTCAA
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NUMBER OF SEQUENCES: 3
CORRESPONDENCE ADDRESS:
ADDRESSE: Marshall, O'Toole, Gerstein, Murray & B
STREET: 6300 Sears Tower, 233 S. Wacker Drive
CITY: Chicago
STATE: 1111nois
COUNTRY: USA
ZATE: 1111nois
COUNTRY: USA
ZIP: 60606
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC COMPATIBLE
OMPUTER: BM PC-DOS/MS-DOS
SOFTWARE: PATENTIN PC-DOS/MS-DOS
SOFTWARE: PATENTIN NATE: 07-JUN-1995
CLASSIFICATION NUMBER: US/08/475,391
FILING DATE: 07-JUN-1995
CLASSIFICATION NUMBER: 08/24,358
FILING DATE: ATPORMATION:
APPLICATION NUMBER: 08/254,358
FILING DATE:
ATLING DATE:
A
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Pred. No. 0;
0; Mismatches 466;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NAME: NO. 5786211and, Greta B.
REGISTRATION NUMBER: 35,302
REBERENCE/DOCKET NUMBER: 31975
TELECOMMUNICATION INFORMATION:
TELEPRA: (312) 474-6300
TELEFAX: 25-3856
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 4680 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1 TOPOLOGY: linear
1 MOLECULE TYPE: DNA (genomic)
US-08-475-391-1
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Best Local Similarity 78.7%;
Matches 1740; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                           466;
                                                                                                                                                                                                                                                                                                                                                       Score 1436.4;
Pred. No. 0;
0; Mismatches
                    TELEPHONE: (312) 474-6300
TELEFAX: (312) 474-0448
TELEX: 25-3856
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 4680 base pairs
TYPE: nucleic acid
  TELECOMMUNICATION INFORMATION
                                                                                                                                                                                                                                             TOPOLOGY: linear MOLECULE TYPE: DNA (genomic)
                                                                                                                                                                                                                                                                                                                                                       65.0%;
                                                                                                                                                                                                                                                                                                                                                                                    Best Local Similarity 78.7
Matches 1740; Conservative
                                                                                                                                                                                            TYPE: nucleic
STRANDEDNESS:
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US-08-709-609-1
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3760 GGGCCGCCATGGCAAGCCACAAGGACGATGAAGAAAAGTTTTTCCTCAGAGCGGGGTT
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                                                                                1621 ATGATTTTTGGAAAAGAGGGCCGGAGCTTCAAACACTGCATTGGACAATGTCATGATT
                                                                                                                           3820 C†CATCTTTGGGAAGCAAGGCTCAGAGAAAACAAATGTGAAACATTGAAAAGGTCATGATT
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Adeno-Associated Virus Materials
Methods
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S. Wacker
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NUMBER OF SEQUENCES:

CORRESPONDENCE ADDRESS:
ADDRESSEE: Marshall, O'Toole, Ge
STREET: 6300 Sears Tower, 233 S.
CITY: Chicago
STATE: 111inois
COUNTRY: USA
ZIP: 60606
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
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NAME: NO. 5888775and, Greea E.
REGISTRATION NUMBER: 35,302
REFERENCE/DOCKET NUMBER: 31975
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 1, Application US/08709609
Patent No. 5858775
GENERAL INFORMATION:
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TITLE OF INVENTION:
TITLE OF INVENTION:
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1 ATGGCTGCCGATGGTTATCTTCCAGATTGGCTCGAGGACAACCTCTCTGAGGGCATTCGC
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                                                                                  1981 GAGTITITCAGCTACAAAGTITGCTTCATTCATCACCCAATACTCCACAGGACA-AGTGAG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 1. Application PC/TUS9507178

GENERAL INFORMATION:
APPLICANT: Johnson, Philip R.
TILLE OF INVENTION: Adeno-Associated Virus Materials and TILLE OF SEQUENCES: 3
CORRESPONDENCE ADDRESS:
ADDRESSEE: ASTERET: 6300 Sears Tower, 233 S. Wacker Drive STREET: Chicago
STREET: Chicago
STATE: Illinois
COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Murray & Borun
Drive
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Pred. No. 0;
0; Mismatches 466; Indels
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MEDIUM TYRER READABLE FORM:
MEDIUM TYRE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/NS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US95/07178
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CLASSIFICATION:
ATTORNEY/AGENT INFORMATION:
NAME: Noland, Greta E.
REGISTRATION NUMBER: 35,302
REFERENCE/DOCKET NUMBER: 31975
TELECOMMUNICATION INFORMATION:
TELEPHONE: (312) 474-6300
TELEPHONE: (312) 474-6300
TELEPHONE: 25-3856
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 4680 base pairs
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Best Local Similarity 78.7%;
Matches 1740; Conservative
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GRAGGAGGAGGAGGAGGAGGAGGAGGAGGAGCCTTCAAAGAGGAGCTTCAAAGCTTCAAAGCTTCAAAGCTTCAACGACTTCAACGACTTCAACGACTTCAACGACTTCAACGACTTCAACGACTTCAACGACTTCAACGACTTCAAAAGCTTCAACGACTTCAAAAGCTTCAACGACTTCAACGACTTCAACGACTTCAACGACTTCAACGACTTCAACGACTTCAACGACTTCAACGACTTCAACGACTTCAACGACTTCAACGACTTCAACGACTTCAACGACTTCAACGACTTCAACGACTTCAACGACTTCACCAACGCTTTCAACGACTTCAACACTTTTAAACGACTTCAACAACTTTTTAAACATTTAAACACTTTAAACACTTTTAAACACTTTTAAACACTTTTAAACACTTTTAAACACTTTTAAACACTTTTAAACACTTTAAAACACTTTAAAACACTTTAAAACACTTTAAAACACTTTAAAACACTTTAAAACACTTTAAAACACTTTAAAACAAC		
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November 28, 2005, 08:46:14; Search time 1033.63 Seconds (without alignments) 14243.261 Million cell updates/sec
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GenCore version 5.1.6
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Listing first 45 summaries
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                                                                                                                                                                                                              Scoring table:
                                                                                                                                                                                Sequence:
                                                                                                                                                                                                                                                         Searched:
                                                                                                                                                                                                                                                                                                                                                                                                                            Database
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

Ad22022 Adeno-ass Ad22692 Adeno-ass Ad26594 HSV-AAV a Ad00772 Adeno-ass Ad67507 Adeno-ass Ad67507 Adeno-ass Ad11394 Adeno-ass Ad26947 Vector pF Ad26947 Vector pF Ad26947 Adeno-ass Ad22693 Adeno-ass Ad22693 Adeno-ass Ad26931 Adeno-ass Ad2693 Adeno-ass Ad27053 Adeno-ass Ad26598 HSV-AAV s Ad26599 Adeno-ass Ad26598 Adeno-ass Ad26598 Adeno-ass Ad26598 Adeno-ass Ad39402 Adeno-ass Ad427053 Adeno-ass Ad39403 Adeno-ass Ad439402 Adeno-ass Aad00777 Adeno-ass Description SUMMARIES ADE76507 ADL13984 ADG39758 ACC58477 ADZ26931 ADZ27053 ADW39402 ADZ46598 AAF23749 ADL13983 ADG39763 ADW39398 ADZ46594 AAD00772 ADZ26928 ADZ26930 ADZ26929 Query Match Length DB 4718 4718 4718 7447 22211 22211 22211 22211 4239 4683 1000 11000 11000 11000 11000 11000 11000 11000 11000 11000 11000 11000 11000 11000 11000 11000 Score 2105 2105 2105 2105 2105 2105 Result No.

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ខូន	F	The patent d	discloses	ев an	adeı	adeno-associated virus s	serotype 1 (AAV-1)	1) DNA

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which is characterised by two inverted terminal repeats (ITR) and open reading frames for rep and capsid (cap) proteins. The rep reading frame encodes four proteins, Rep 78, Rep 68, Rep 52 and Rep 40, while the cap reading frame encodes three structural proteins, VPI, VP2 and VP3. The AAV-1 sequence or its fragments particularly ITRs, rep and cap coding regions, are useful in production of recombinant viral vectors for gene
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regions, are useful in production of recombinant viral vectors for gene delivery. These vectors can be used as gene therapy vectors, vaccine vectors or antisense delivery vectors. The AAV-1 does not induce the formation of neutralising antibodies specific to any serotype of AAV hence is useful for transforming host cells, and in the preparation of a medicament for the dalivery of transgene to a host. The present sequence is an AAV-1 DNA encoding a cap protein VP1 which is useful in the production of recombinant viral vector for gene delivery Sequence 2211 BP; 577 A; 652 C; 538 G; 444 T; 0 U; 0 Other;	uery Match 100.0%; Score 2209; DB 3; Length 2211; est Local Similarity 100.0%; Pred. No. 0; atches 2209; Conservative 0; Mismatches 0; Indels 0; Gaps 0;	1 ATGGCTGCCGATGGTTATCTTCCAGATTGGCTCGAGGACAACCTCTCTGAGGGCATTCGC 60	61 GAGTGGTGGGACTTGAAACCTGGAGCCCCGAAGCCAAAGCCAACCAGCAAAAGCAGGAC 120 	121 GACGGCGGGGTCTGGTGCTTCTGGCTACAATACCTCGGACCCTTCAACGGACTCGAC 180	181 AAGGGGAGCCCGTCAACGCGGCGGACCGGCCCCTCGAGCACGACAAGGCCTACGAC 240	241 CAGCAGCTCAAAGCGGGTGACAATCCGTACCGGTATAACCACGCCGACGCCGAGTTT 300 	301 CAGGAGCGTCTGCAAGAAGATACGTCTTTTGGGGGGAACCTCGGGCGAGCAGTCTTCCAG 360 	361 GCCAAGAAGGGGGTTCTCGAACCTCTCGGTCTGAGGAAGGCGCTAAGACGGCTCCT 420 	421 GGAAAGAACGTCCGGTAGAGCAGTCGCCACAAGAGCCAGACTCCTCCTCGGGCATCGGC 480	481 AAGACAGGCAGCAGCTAAAAAGAGACTCAATTTTGGTCAGACTGGCGACTCAGAG 540 	541 TCAGTCCCGGATCCACAACCTCTCGGAGAACCTCCAGCAACCCCGGTGCTGTGGGACCT 600	601 ACTACAATGGCTTCAGGCGGTGGCGCACCAATGGCAACAATAACGAAGGCGCCGACGGA 660 	661 GTGGGTAATGCCTCAGGAAATTGGCATTGCGATTCCACATGGCTGGGCGACAGAGTCATC 720	721 ACCACCAGCACCGGACCTGGCCCACCTACAATAACCACTCTACAAGCAATC 780 	781 TCCAGTGCTTCAACGGGGGCCAGCAACGACAACTACTTCGGCTACAGCACCCCTGG 840

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<u>ک</u> ۾	901	ATCAACAACAATTGGGGATTCCGGCCCAAGAGACTCAACTCTTCAACATCTACAA 960
<i>장</i>	961	GTCAAGGAGGTCACGACGAATGATGGCGTCACAACCATCGCTAATAACCTTACCAGCACG 1020
ठे त	1021	GTTCAAGTCTTCTCGGACTTCCGAAGTACCAGCTTCCGTACGTCCTCGGCTCTGCGCACCAG 1080
}	1081	114
Db	1081	114
දු දු	1141	CTCAACAATGGCCGCGCGGGGGGGGGTTCATCCTTTTACTGCCTGGAATATTTCCCT 1200
ું ક	1201	TCTCAGATGCTGAGAACGGGCAACAACTTTACCTTCAGCTACACCTTTGAGGAAGTGCCT 1260
3 8	1021	1 2 3
· 유	1261	TTCCACACACCACACACACACACACACACACACACACAC
ò	1321	CAATACCTGTATTACCTGAACAGAACTCAAAATCAGTCCGGAAGTGCCCAAAACAAGGAC 1380
3 8	1381	144
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ò	1441	20
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e s	1501	TTTACCTGGACTGGTGCTTCAAAATATAACCTCAATGGCGTGAATCCATCATCAACCT 1560
È	1561	62
a a	1561	162
å å	1621	ATGATTTTTGGAAAAGAGGGCGGGGGGCTTCAAACACTGCATTGGACAATGTCATGATT 1680
È	1681	ACAGACGAAGAAGAAATTAAAGCCACTAACCCTGTGGCCACCGAAAGATTTGGGACCGTG 1740
qq	1681	ACAGACGAAGAGGAAATTAAAGCCACTAACCCTGTGGCCACCGAAAGATTTGGGACGACGTG 1740
රු ජ	1741	GCAGTCAATTTCCAGAGCAGCAGCACAGACCCTGCGACCGGAGATGTGCATGCTATGGGA 1800 ACAGCAAGTTAATTTCAAAAAAAAAAAAAAAAAAAAAAA
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상 옵	1801	GCATTACCTGGCATGGTGGCAAAATAGAGACGTGTGGGGGGGTCCCATTGGGCC 186 GCATTACCTGGCATGGTGTGGCAAGATAGAGACGTGTACCTGCAGGGTCCCATTTGGGCC 186
λΌ	1861	AAAATTCCTCACACAGATGGACACTTTCACCCGTCTCCTTATGGGCGGCTTTGGACTC 1920

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 colitis. The present sequence represents an adeno-associated
                              Seguence 2211 BP; 577 A; 652 C; 538 G; 444 T; 0 U; 0 Other;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             rheumatoid arthritis; multiple sclerosis; sarcoidosis; diabetes; scleroderma; psoriasis; vasculitis; Crohn's disease; hemophilia; HIV; bacterial infection; cancer; ulcerative colitis; antrheumatic; antiathritic; neuroprotective; antiidlammatory; antidibetic; antipporiatic; vasotropic; gastroincestinal-gen.; hemostatic; anti-HIV; virucide; antibacterial; cytostatic; antiulcer; dermatological; ds.
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    1861 AAAATTCCTCACACAGATGGACACTTTCACCCGTCTCCTCTTATGGGCGGCTTTGGACTC
                                                             AAGAACCCGCCTCCTCATCCATCAAAACACGCCTGTTCCTGCGAATCCTCCGGCG
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29-APR-2004; 2004US-0566546P.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 The invention relates to a novel recombinant herpes simplex virus (rHSVS) whose genome is respectively inserted by the Adeno-associated virus (AAV) rep gene and cap gene. The AVV genes may be derived from viruses AAVI, AAV2, AAV3, AAV4, AAV5 and AAV6. The methods of the invention may be useful for generating recombinant vectors with high efficiency and no need of reconfiguration. The current sequence is that of the Adeno-associated virus 2 (AAV2) rep-Adeno-associated virus 1 (AAV1) cap fusion
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Structure of a recombinant herpes simplex virus and its use
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                                                                                                                                               fusion DNA
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ilarity 100.0%; Pred. No. 0;
Conservative 0; Mismatches
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                        ВР
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                          standard; DNA; 4347
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                                                                                                                                                                                                                                                                                                                                                                                                                           27-MAY-2002; 2002CN-00117965
                                                                                                       entry)
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                                                                                              3581 GGCACTGCTATGGCCTCACACAAGACGACGAAGACAAGTTCTTTCCCATGAGGGGTGTC
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gene therapy; vector; cancer; neoplasm; cytostatic; respiratory-gen.; neurological disease;
                                                               HSV-AAV sequence rep2cap1 for AAV/HSV vectors.
       ВР
       ADZ46594 standard; DNA; 4347
                                            (first entry)
                                                                                                                        Adeno-associated virus.
                                                                                   Genetic engineering; respiratory disease;
                                                                                                     neuroprotective; ds.
                                                                                                                                  Human herpesvirus 1.
                                           30-JUN-2005
                          AD246594;
ADZ46594
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1 ATGGCTGCCGATGGTTATCTTCCAGATTGGCTCGAGGACAACCTCTGAGGGCATTCGC

Length 4347;

DB 14;

Sequence 4347 BP; 1106 A; 1186 C; 1142 G; 913 T; 0 U; 0 Other;

.. 0

0; Indels

0; Mismatches 100.0%; Score 2209; 100.0%; Pred. No. 0;

Best Local Similarity 100. Matches 2209; Conservative

Query Match

2081 GAGTGGTGGGACTTGAAACCTGGAGCCCCGAAGCCCAAAGCCAACCAGCAAAAGCAGGAC

GACGGCCGGGGTCTGGTTCCTGGCTACAAGTACCTCGGACCCTTCAACGGACTCGAC

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61 GAGTGGTGGGACTTGAAACCTGGAGCCCCGAAGCCCAAAGCCAAAAGCAAGGAAC

2141 gacggccggggrcriggrgcrrccrggcracaagraccrcggaccrrcaacgacrcgac AAGGGGGAGCCCGTCAACGCGGCGGACGCAGGGCCCTCGAGCACGACAAGGCCTACGAC AAGGGGGAGCCCGTCAACGCGGCGGACGCAGGGCCCTCGAGGCACGACAAGGCCTAACGAC CAGCAGCTCAAAGCGGGTGACAATCCGTACCTGCGGTATAACCACGCCGACGCCGAGTTT 2320

2201 181

241

15-OCT-2003; 2003WO-CN000861.

21-APR-2005

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The invention relates to a recombinant herpes simplex virus (HSV)

Characterized in that its genome is inserted with a DNA sequence selected

Characterized in that its genome is inserted with a DNA sequence selected

Characterized in that its genome is inserted with a DNA sequence selected

Erom nucleotide sequences of ADZ46594 or their homologous

CC sequences. Also included are preparing the recombinant HSV, inserved

BNY applying genetic engineering to give the recombinant HSV, inserved

Exale production of S serotype recombinant dehos—associated viruses (AAV)

CC scale production of S serotype recombinant thsV, establishing a one-

series production of S serotype recombinant HSV, establishing a one-

corresponding vector cell-line with the S recombinant HSV, producing

corresponding vector cell-line with the S recombinant HSV in the corresponding vector cell-line, separating and purifying the S serotype recombinant

CC AAV after lysing the AAV-containing cells and culture liquor to give a crude lysate and further purification of rAAV by density-gradient

CC AAV after lysing the AAV-containing cells and culture liquor to give a crude lysate and further purification of rAAV by density-gradient

CC Chamegalovirus, and a polyclonal site and a recombinant vector, pleasmid pSNAV-NX (containing ITR at both enda competer of the cypressing cassette at outer edge of ITR). The DNA sequence of into XDA sequence ADZ46594 can also be inserted into other non-essential caste for use in gene therapy of e.g. cancer, respiratory diseases and neural diseases. The virus vectors are safe, with long expression time and wide-spectrum of cell infection, even non-clawed cells and reverse axonal conduction through the incorporated HSV vectors, and high transfer efficiently. The present sequence is the HSV-ANV and high transfer efficiently. The present sequence is the HSV-ANV and high transfer efficiently. The present sequence is the present sequence of cells and reverse axonal conduction through the present sequence is the present se
                                                                                                                                                                                                                                         Large-scale production, isolation and purification of serotype adeno-
associated virus vectors by infecting cells with recombinant herpes
simplex virus vectors, for use in gene therapy of e.g. cancer and
                                                                                                                                                                                                                                                                                                                                                                                                                                       The invention relates to a recombinant herpes simplex virus (HSV)
                                                                             (AGTC-) AGTC GENE TECHNOLOGY CO LTD.
                                                                                                                                                                                                                                                                                                                                                                                      Claim 1, SEQ ID NO 1, 79pp; Chinese.
                                                                                                                                    Cao H, Dong X;
                                                                                                                                                                                                                                                                                                                          respiratory diseases.
                                                                                                                                                                                           WPI; 2005-296279/30.
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1381 TTGCTGTTTAGCCGTGGGTCTCCAGCTGTTCTGTTCTGCCCAAAACTGGCTACCT 1440	Db 3581 GGCATTATTATGGAAAAGAGACAAATTCTTTTCCATTGAGGGTTTTTTTT	Qy 1741 GCAGTCAATTCCAGAGCAGCACAGACCCTGCGACCGGAGATGTGCATGCTATGGGA 1800 Db 3761 GCAGTCAATTTCCAGAGCAGCACAGCACCTGCGACCGGAGATGTGCATGCTATGGGA 3820 Qy 1801 GCATTACCTGGCATGGTGGCAAGATGAGAGACGTGTACCTGCAGGTCCCATTTGGGC 1860 Db 3821 GCATTACCTGGCATGGTGGCAAGATAGAGACGTGTACCTGCAGGGTCCCATTTGGGC 3880	QY 1861 AAAATTCCTCACACACAGATGGACACTTTCACCCGTCTCTTATGGGCGGCTTTGGACTC 1920 Db 3881 AAAATTCCTCACACAGATGGACACTTTCACCGGTCTCTTATGGGCGGCTTTTGGACTC 3940 QY 1921 AAGAACCCGCCTCCTCAGATCCTCAAAAACACGCCTGTTCCTGCGAATCCTCCGGCG 1980 Db 3941 AAGAACCCGCCTCCTCAGATCCTCATCAAAAACACGCCTGTTCCTGCGAATCCTCCGGCG 4000	OY 1981 GAGTTTTCAGCTACAAAGTTTGCTTCATCACCCAATACTCCACAGGACAAGTGAGT 2040	Oy 2101 TACACATCCAATTATGCAAAATCTGCCAACGTTGATTTTACTGTGGACAACAATGGACTT 2160	RESULT 6 AAD00772 ID AAD00772 standard; DNA; 4718 BP. XX AC AAD00772; XX XX DT 08-SEP-2000 (first entry)	XX XX XX XX XX XX XX XX XX KW Adeno-associated virus serotype 1, AAV-1; rep protein; capsid protein; KW cap protein; recombinant viral vector; gene delivery; gene therapy; XX
888888	a 6 a 6 a	<i>៩ គ 6</i>	ଟ ବି ଚି ଗି	8	8888		
301 CAGGAGCGTCTGCAAGAAGATACGTCTTTTGGGGGCAACCTCGGGCGAGCAGTCTTCCAG 360 2321 CAGGAGCGTCTGCAAGAAGATACGTCTTTTGGGGGCAACCTCGGGGGACAGTCTTCCAG 2380 361 GCCAAGAGCGGGTTCTCGAACCTCTCGGTTGAGGAGCGGTAAGACGCTTTCCAG 2380 361 GCCAAGAACGGGTTCTCGAACCTCTCGGTTGAGGAGCGCTAAGACGGCTCT 420 421 GGAAAGAAACGGGTTCTCGAACCTCTCGGTTGAGGAGCGCTAAGACGGCTCCT 2440 421 GGAAAGAAACGTCCGGTAGAACGTCGCCACAAGAGCCCAGACTCCTCCGGGCATCGGC 480 [AGACCAGCAGCAGCCGCTAAAAAGAGACCCCAATTTTGGTCAGACCTCAGAG AAGACCAGCCGGCCGCTAAAAAGAGACTCAATTTTGGTCAGACCTGGCGACTCAGAG TCAGTCCCCGATCCACAACCTCTCGGAGAACCTCCAGCAACCCCCGCTGCTGTGGGACCT TCAGTCCCCGATCCACAACCTCTCGGAGAACCTCCAGCAACCCCCGCTGCTGTGGGACCT ACTACAATGGCTTCAGGCGGTGGCGCACCAATGACGAAAAAACGAAGACGCCGAACGA			ATCAACAACAATTGGGGATTCCGGCCCAAGAGACTCAACTTCAACTTCAACATCCAA TCAACAACAATTGGGGATTCCGGCCCAAGAGCTCAACTTCAAACTCTTCAACATCCAA GTCAACAACAAGAGGTCACGAGGGGTCAACTTCAACTTCAACTTCCAACTTCCAA GTCAAGGAGGTCACGACGAATGATGGGGTCACAACACATGGTTAATAACCTTAACAGCACCATCGCTAATAACACAACAAGAGGTCAACAACAACAACAACAACAACAACAACAACAACAACAA		1141 CTCAACAATGGCAGCCAAGCCGTTCATCCTTTTACTGCCTGGAATATTTCCCT 1200	1261 TTCCACAGCAGCTACGCGCACAGCCTGAACCGGCTGATGAATCCTCTCATCGAC 1320

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2463 CAGCAGCTCAAAGCGGGTGACAATCCGTACCGGGTATAACCACGCCGACGCCGAGTTT 2522
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                                                                                                                                                                                                                                                                                                                                                                                                                                   The present sequence is an adeno-associated virus serotype 1 (AAV-1) DNA characterised by two inverted terminal repeats (ITR) and open reading frames for rep and capsid (cap) proteins. The rep reading frame encodes four proteins, Rep 78, Rep 68, Rep 52 and Rep 40, while the cap reading frame encodes three structural proteins, VP1, VP2 and VP3. The AAV-1 are useful in production of recombinarly ITRs, rep and cap coding regions, are useful in production of recombinant viral vectors for gene delivery. These vectors can be used as gene therapy vectors, vaccine vectors or antisense delivery vectors. The AAV-1 does not induce the formation of neutralising antibodies specific to any serotype of AAV hence is useful for transforming host cells, and in the preparation of a medicament for the delivery of transgene to a host
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                GAGTGGTGGGACTTGAAACCTGGAGCCCCGAAGCCCAAAAGCCAAAAAGCAGGAC
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                                                                                                            /*tag= v
/label= 1'ITR
/note= "inverted terminal repeat which is capable of
forming T-shaped hairpin structure"
                                                                                                                                                                                                                                                                                                                           WPI; 2000-376571/32.
P-PSDB; AAY71161, AAY71164, AAY71165, AAY71166, AAY71167, AAY71168.
                                                                                                                                                                                                                                                                                                                                                                        Novel adeno-associated virus serotype 1 polynucleotide useful for preparation of medicament for delivery of a transgene to a host.
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100.0%; Pred. No. 0;
:ive 0; Mismatches
                                        /product= "VP3 protein"
/note= "Capsid protein"
4447. .4452
"Capsid protein"
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                  /*tag= t
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Matches 2209; Conservative
          partial
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note= "This region interrupts the coding sequence of Rep
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function= "regulates replication and integration of AAV
NA into host cell's chromosome"
                                                                                                                                                                                                                                                                                                                                                                                          replication and integration of AAV
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function= "regulates replication and integration of AAV
                       /*tag= a
//abel= 5'_ITR
//note= "Inverted terminal repeat which is capable of
forming T-shaped hairpin structure"
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note= "The coding region is interrupted by intron"
007. .2206
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note= "Terminal resolute site (TRS)"
                                                                                    *tag= b
bound moiety= "Rep protein"
124. .125
                                                                                                                                                                                                                                                  *tag= f
bound moiety= "YY1 factor"
270. .275
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ipsid protein"
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/note= "E box"
236. .299
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/note= "YY1/p5 RNA"
335. .2272
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label= P19_TATA_Box
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label= P40_TATA-BOX
875. .1876
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label= P5_promoter
37. .245
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label= P5_TATA-Box
Location/Qualifiers
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product= "Rep 78"
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note= "P40 RNA"
924. .2220
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634. .4433
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                                                                           2643 GGAAAGAAACGTCCGGTAGAGCAGTCGCCACAAGAGCCAGACTCCTCCTCGGGCATCGGC
                                                                                                                              481 AAGACGCCAGCAGCCCCTAAAAAGACACTCAATTTTGGTCAGACTGGCGACTCAGAG
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                                                        GGAAAGAAACGTCCGGTAGAGCAGTCGCCACAAGAGCCCAGACTCCTCCGCGCCATCGGC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                DB 10; Length 4718;
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1larity 100.0%; Pred. No. 0;
Conservative 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                Claim 14; SEQ ID NO 6; 419pp; English.
                                                                                                                                                                  13-NOV-2001; 2001US-0350607P.
17-DEC-2001; 2001US-0341117P.
01-MAY-2002; 2002US-037066FP.
05-JUN-2002; 2002US-0386675P.
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                                                                             GGCACTGCTATGGCCTCACACAAGACGACGAAGACAAGTTCTTTCCCATGAGCGGTGTC
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                      TTTACCTGGACTGGTGCTTCAAATATATAACCTCAATGGGCGTGAATCCATCATCAACCCT
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The invention relates to an expression construct comprising a nucleic acid sequence encoding an adeno-associated virus integration efficiency element (AAV INTES), which is devoid of AAV inverted terminal repeats (AAV ITRS) and site-specifically integrates into a host cell chromosome when provided to the host cell in conjunction with an AAV Rep protein. The expression construct can be used as a therapeutic factor for treating a mammal for a pathologic state which is cancer, including lung cancer, colon cancer, brain cancer, bile duct cancer, bladder cancer, brain cancer, spinal chord cancer, bladder cancer, yastrointestinal cancer, laryngeal cancer, pathologic salibladder cancer, esophageal cancer, prostatic cancer, esophageal cancer, prostatic cancer, estinolastoma, neuroblastoma, ovarian cancer, panceatic cancer, prostatic cancer, thymas cancer or thyroid cancer. Other pathologic state includes inflammatory disease (arthritis), neurodegenerative catering a disease of an organ attributed to the presence of increased or decreased level of a particular gene product(8). This sequence concernesponds to the AAV serotype I complete DNA including the IEE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Indels
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100.0%; Score 2209;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 2209; Conservative 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Disclosure; SEQ ID NO 3; 62pp; English
                                                                                                                                                                                                                              Philpott N;
09-APR-2003; 2003WO-US011191.
                                                                          09-APR-2002; 2002US-0371044P.
                                                                                                                                                                                                                                                                                                        WPI; 2003-833723/77
                                                                                                                                                                                                                                  Falck-Pedersen ES,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    e.g. arthritis.
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421 GGAAAGAAACGTCCGGTAGAGCAGTCGCCACAAGAGCCAGACTCCTCCTCGGGCATCGGC 480

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WO2003087334-A2

23-OCT-2003

	1521 TTTACCTGGACTGGACGACGACGACGACGACGATCCTTCCCATGACGGTGTC	RESULT 9 ADG39758 TID ADG39758 standard; DNA; 4718 BP. XX
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The present invention describes a polynucleotide (1), comprising parvovirus rep coding sequences and parvovirus cap coding sequences encodes a DNA binding domain from a first parvovirus, and a capsid interacting domain from a parvovirus different parvovirus. Also described: (1) a vector comprising (1); or parvovirus rep coding sequences from the different parvovirus. Also described: (1) a vector comprising (1); or parvovirus rep coding sequences and parvovirus cap coding sequences, where the rep coding sequences are first parvovirus and a capsid interacting coding sequences comprise sequences from the different parvovirus, and the rep coding sequences are stably integrated into the genome of the coding sequences are stably integrated into the genome of the cell; and (3) producing a recombinant hybrid parvovirus particle or adenocasociated virus (rAAV) particle. (1) can be used in producing higher socks of hybrid parvoviruses or parvovirus vectors, which may be used in the delivery of nucleic acides having biological effect to treat or ammiliorate the symptoms associated with any disorder related to gene expression. The polynucleotide may be used to produce a parvovirus vector or ammiliorate the symptoms associated with any disorder related to gene expression. The polynucleotide may be used to produce a parvovirus vector or expression. The polynucleotide may be used to produce a parvovirus vector companion to paramore in a subject, eagl for vaccination. The parvovirus vector may also be used to provide an antisense nucleic may and the methods. The present sequence is used in the exemplification of the manner of the contraction of the manner 
                                                                                                                                          New polynucleotides comprising parvovirus rep coding sequences and parvovirus cap coding sequences, useful in producing higher stocks of hybrid parvovirus vectors for delivering therapeutic nucleic acids to subject.
                                                                                                                                                                                                                                                                                                                                          Disclosure; SEQ ID NO 20; 115pp; English.
                                                                                               WPI; 2004-062324/06.
                            Samulski RJ,
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Sequence 4718 BP; 1121 A; 1393 C; 1273 G; 931 T; 0 U; 0 Other;

2282 2402 2462 2522 2582 2642 240 420 480 120 180 300 360 ATGCCTGCCGATGGTTATCTTCCAGATTGGCTCGAGGACAACCTCTCTGAGGGCATTCGC dacadecedadarerrectederracaagraceredadecerreaacedacredae AAGGGGGAGCCCGTCAACGCGGGCGGCGCGCCCTCGAGGCACGACAAGGCCTACGAC CAGCAGCTCAAAGCGGGGTGACAATCCGTACCTGCGGTATAACCACGCCGACGCCGACGTTT CAGGAGCGTCTGCAAGAAGATACGTCTTTTGGGGGCAACCTCGGGCGAGCAGTCTTCCAG CAGGAGCGTCTGCAAGAAGATACGTCTTTTGGGGGCAACCTCGGGCGAGCAGTCTTCCAG GCCAAGAAGCGGGTTCTCGAACCTCTCGGTCTGGTTGAGGAAGGCGCTAAGACGCTCCT 1583 GCCAAGAAGCGGGTTCTCGAACCTCTCGGTCTGGTTGAGGAAGGCGCTAAGACGGCTCCT GGAAAGAAACGTCCGGTAGAGCAGTCGCCACAAGAGCCAGACTCCTCCTCGGGCATCGGC **AAGGGGGGCCCGTCAACGCGGCGGACGCAGCGGCCCTCGAGCACGACAAGGCCTACGAC** CAGCAGCTCAAAGCGGGTGACAATCCGTACCTGCGGTATAACCACGCCGACGCCGAGTTT ATGGCTGCCGATGGTTATCTTCCAGATTGGCTCGAGGACAACCTCTCTGAGGGCATTCGC GACGGCCGGGGTCTGGTGCTTCCTGGCTACAAGTACCTCGGACCCTTCAACGGACTCGAC Gaps Length 4718; ö Indels DB 12; .; 0 100.0%; Score 2209; larity 100.0%; Pred. No. 0; Conservative 0; Mismatches Query Match Best Local Similarity Matches 2209; Conserv 2223 2343 2403 241 2463 2523 361 Н 121 181 61 301 421 名 셤 셤 ò g a 8 유 ઠ ò ò ò ò ઠે

3782

3362 1200 1260 3482 3182 2942 3062 3122 GITCAAGTCTTCTCGGACTCGGAGTACCAGCTTCCGTACGTCCTCGGCTCTGCGCACCAG 1080 2822 3002 540 99 720 840 900 960 780 3543 CAATACCTGTATTACCTGAACAGAACTCAAAATCAGTCCGGAAGTGCCCAAAAACAAGGAC GGACCCTGTTATCGGCAGCAGCGCGTTTCTAAAACAAAAACAGACAACAACAACAACAAT 3723 TTTACCTGGACTGGTGCTTCAAAATATAACCTCAATGGGCGTGAATCCATCATCATCACCT 2703 AAGACAGGCCAGCAGCCCGCTAAAAAGAGACTCAATTTTGGTCAGACTGGCGACTCAGAG GTGGGTAATGCCTCAGGAAATTGGCATTGCGATTCCACATGGCTGGGCGACAGAGTCATC 3063 GGGTATTTGATTTCAACAGATTCCACTGCCACTTTTCACCACGTGACTGGCAGCGACTC ATCAACAATTGGGGATTCCGGCCCAAGAGACTCCAACTTCAAACTCTTCAACATCAACAACAA GTCAAGGAGGTCACGACGAATGATGGCGTCACAACCATCGCTAATAACCTTACCAGCACG GTCAAGGAGGTCACGACGAATGATGGCGTCACAACCATCGCTAATAACCTTACCAGCACG GTTCAAGTCTTCTCGGACTCGGAGTACCAGCTTCCGTACGTCCTCGGCTCTGCGCACCAG GGCTGCCTCCCTCCGGTGCGGGGGGGGGGTTCCATGATTCCGCAATACGGCTACCTGACG Gectecetecetecedatecedaedaedateatataedaataedeetaeetaaed CAATACCTGTATTACCTGAACAGAACTCAAAATCAGTCCGGAAGTGCCCAAAACAAGGAC TTGCTGTTTAGCCGTGGGTCTCCAGCTGGCATGTCTGTTCAGCCCAAAAACTGGCTACCT Trigorientragicionegoriente de contraction de la TTTACCTGGACTGGTGCTTCAAATATAACCTCAATGGGCGTGAATCCATCAACCCT 2643 GGAAAGAAACGTCCGGTAGAGCAGTCGCCACAAGAGCCAGACTCCTCCTCGGGCATCGGC ACTACAATGGCTTCAGGCGGTGGCGCACCAATGGCAGACAATAACGAAGGCGCCGACGGA GTGGGTAATGCCTCAGGAAATTGGCATTGCGATTCCACATGGCTGGGCGACAGAGTCATC ACCACCAGCACCCGCACCTGGGCCTTGCCCACCTACAATAACCACCTCTACAAGCAAATC **ATCAACAACAATTGGGGATTCCGGCCCAAGAGACTCCAACTTCAAACTCTTCAACATCCAA** CTCAACAATGGCAAGCCGTGGGACGTTCATCCTTTTACTGCCTGGAATATTTCCCT rereagardergagaacgggcaacaacrrraccrrcagcracaccrrraaggaagracer **AAGACAGGCCAGCAGCCCGCTAAAAAGAGACTCAATTTTGGTCAGACTGGCGACTCAGAG** TCAGTCCCCGATCCACAACCTCTCGGAGAACCTCCAGCAACCCCCGCTGCTGTGGGACCT ACTACAATGGCTTCAGGCGGTGGCGCACCAATGGCAGACAATAACGAAGGCGCCGACGGA ACCACCAGCACCTGGGCCTTGCCCACCTACAATAACCACCTCTACAAGCAAATC TCCAGTGCTTCAACGGGGCCAGCAACGACAACCACTACTTCGGCTACAGCACCCCTGG GGGTATTTTGATTTCAACAGATTCCACTGCCACTTTTCACCACGTGACTGGCAGCGACTC crcaacaarogcagccaagccgrogaacgricarccrrrrracrgccrogaararrrcccr TCTCAGATGCTGAGAACGGGCAACATTTACCTTCAGCTACACCTTTGAGGAAGTGCCT 2823 2883 2943 3003 3123 3183 1021 1081 3303 1141 3363 1201 3423 1261 3483 1321 1381 3603 1441 3663 1501 2763 601 721 781 901 481 541 661 841 961 3243 셤 유 요 ò g ò 윰 ठे g ò ያ ያ ద 8 8 8 셤 ò 셤 ò 셤 ò 유 ò 셤 ò 셤 ò 셤 ò 셤 ò ò ð ઠે

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The present sequence is that of vector pFBDAAV1-VP, which comprises a modified adeno associated virus serotype 1 (AAV1) VP capsid gene. The modified vP gene has the VPI initiation codon mutated to AGG to reduce its translation efficiency. An out-of-frame ATG, which diminishes the translation of VP2 and VP3, is also modified, and the splice acceptor site downstream of the VP1 initiation codon has been destroyed. Recombinant baculovirus vectors comprising the mutant AAV1 VP gene were produced from pFBDAAV1-VP for use in the production of recombinant AAV particles comprising AAV1 capsid proteins in insect (Sf9) cells. The method of producing AAV in insect cells provides an efficient, safe and economical means of producing a large amount of recombinant AAV particles which may be used in gene therapy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           4741 GACGGCCGGGGTCTGGTGCTTCCTGGCTACAGTACCTCGGACCCTTCAACGGACTCGAC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1 ATGGCTGCCGATGGTTATCTTCCAGATTGGCTCGAGGACAACCTCTCTGAGGGCATTCGC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TCAGTCCCCGATCCACAACCTCTCGGAGAACCTCCAGCAACCCCCGCTGCTGGGACCT
                                                      Producing an adeno-associated virus (AAV) in an insect cell, e.g. for gene therapy, comprises introducing an insect cell-compatible vector an insect cell and maintaining the insect cell under conditions that produce AAV.
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                                                                                                                                                                    English
                                                                                                                                                                    Example 7; Page 68-72; 84pp;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match 99.7%;
Best Local Similarity 99.8%;
Matches 2205; Conservative
                    2003-449568/42
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         3783 GGCACTGCTATGGCCTCACAAAGACGACGAAGACAAGTTCTTTCCCATGAGCGGTGTC
                                                                                                                                3843 ATGATTTTTGGAAAAGAGGGCCGGAGCTTCAAACACTGCATTGGACAATGTCATGATT
                                                                                                                                                                                                                                                                                                                                                                                                                                                          AAAATTCCTCACACAGATGGACACTTTCACCCGTCTCCTCTTATGGGCGGCGCTTTGGACTC
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                                                                                                                                                                                             ACAGACGAAGAGAAATTAAAGCCACTAACCCTGTGGCCACCGAAAGATTTGGGACCGTG
                                                                                                                                                                                                                                                                                                                                                                       GCATTACCTGGCATGGTGTGGCAAGATAGAGACGTGTACCTGCAGGGTCCCATTTGGGCC
                                                                                                                                                                                                                                                                                                                                                                                             GCATTACCTGGCATGGTGTGGCAAGATAGAGACGTGTACCTGCAGGGTCCCATTTGGGCC
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                                                                                                                                                                                                                                                                                                          3963 GCAGTCAATTTCCAGAGCAGCACCAGACCCTGCGACCGGAGATGTGCATGCTATGGA
                                                                                                          ATGATTTTTGGAAAAGAGGGCCGGAGCTTCAAACACTGCATTGGACAATGTCATGATT
                                                                                                                                                                                                                                                                                 GCAGTCAATTTCCAGAGCAGCACACAGACCCTGCGACCGGAGATGTGCATGCTATGGGA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        pFBDAAV1-VPP with adeno associated virus 2 VP capsid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AAV; pFBDAAV1-VPP; capsid; insect; gene therapy; vector;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           (USSH ) US DEPT HEALTH & HUMAN SERVICES.
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13-AUG-2002; 2002US-00216870.
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The invention relates to an adeno-associated virus (AAV) clade comprising at least three AAV members, where each member of the AAV clade is phylogenetically related as determined using a Neighbor-Joining heuristic by a bootstrap value of at least 75 \ \forall per 1000 isolates and a Poisson correction distance measurement of no more than 0.05. The methods and compositions of the present invention are useful for the prevention and/or treatment of rheumatoid arthritis, multiple sclerosis, andort treatment of alebetes, scleroderma, psoriasis, vasculitis, Crohn's disease, hemophilia, HIV, bacterial infection, cancer and ulcerative colitis. The present sequence represents an adeno-associated virus DNA.
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Best Local Similarity 99.6%;
Matches 2201; Conservative
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                Score 2124;
Pred. No. 0;
                96.24;
               Query Match
Best Local Similarity 97.8
Matches 2164; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                            rheumatoid arthritis; multiple sclerosis; sarcoidosis; diabetes; scleroderma; psoriasis; vasculitis; Crohn's disease; hemophilia; HIV; bacterial infection; cancer; ulcerative colitis; antirheumatic; antiarthritic; neuroprotective; antillammatory; antidiabetic; antipporiatic; vasotropic; gastroinestinal-gen.; hemostatic; anti-HIV; virucide; antibacterial; cytostatic; antiulcer; dermatological; ds.
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TACACATCCAATTATGCAAAATCTGCCAACGTTGATTTTACTGTGGACAACAATGGACTT
                                             GAGTTTTCAGCTACAAAGTTTGCTTCATCACCCAATACTCCACAGGACAAGTGAGT
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                                                                                                                                                                                             2101 TACACATCCAATTATGCAAATCTGCCAACGTTGATTTTACTGTGGACAACAATGGACTT
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                                                                                                                                                                                                                                          2161 TATACTGAGCCTCGCCCCATTGGCACCCGTTACCCTTACCCGTCCCTGT 2209
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                                                                                 rheumatoid arthritis; multiple sclerosis; sarcoidosis; diabetes; scleroderma; psoriasis; vasculitis; Crohn's disease; hemophilia; HIV; bacterial infection; cancer; ulcerative colitis; antirheumatic; antiarthritic; neuroprotective; antiinflammatory; antidbabetic; antipporiatic; vasotropic; gastroincestinal-gen.; hemostatic; anti-HIV; virucide; antibacterial; cytostatic; antiulcer; dermatological; ds.
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95.3%; Score 2105; DB 14; Length 2211;
Best Local Similarity 97.1%; Pred. No. 0;
Matches 2144; Conservative 0; Mismatches 65; Indels 0:
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                                                       Adeno-associated virus DNA SEQ ID NO 203
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29-APR-2004; 2004US-0566546P.
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                             entry)
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                           30-JUN-2005
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                                                                                                                                                                                                                                                                The invention relates to a novel recombinant herpes simplex virus (rHSVS) whose genome is respectively inserted by the Adeno-associated virus (AAV) rep gene and cap gene. The AVV genes may be derived from viruses AAVI, AAV2, AAV3, AAV4, AAV5 and AAV6. The methods of the invention may be useful for generating recombinant vectors with high efficiency and no associated virus 2 (AAV2) rep-Adeno-associated virus 1 (AAV2) rep-Adeno-associated virus 1 (AAV1) cap fusion DNA (SEQ ID 5) of the invention.
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                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 4239 BP; 1084 A; 1156 C; 1130 G; 869 T; 0 U; 0 Other;
                                                                                                                                                                                                           Structure of a recombinant herpes simplex virus and
                                                                                                                                                                                                                                                                                                                                                                                                                                       DB 13;
                                                                                                                   (BENY-) BENYUAN ZHENGYANG GENETIC TECHNOLOGY
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95.3%; Score 2105; D
Best Local Similarity 97.1%; Pred. No. 0;
Matches 2144; Conservative 0; Mismatches
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                                                         27-MAY-2002; 2002CN-00117965.
                                                                                      27-MAY-2002; 2002CN-00117965
                                                                                                                                                 Cao H, Dong X;
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CN1461805-A
                            17-DEC-2003
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              TIGCTOTITAGCCGGGGGTCTCCAGCTGGCAFGTCTGTTCAGCCCAAAAACTGGCTACCT
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Wilson,J.M. and Xiao,W.
Adeno-associated virus serum type 1 nucleic acid sequence, vector and host cell containing the same
Patent: JP 2002239098-A 6 10-SEP-2002;
THE TRUSTEES OF THE UNIVERSITY OF PENNSYLVANIA
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02-NOV-1999 JP 2000581227
05-NOV-1998 US 60/107114
JAMES M WILSON, WEIDONG XIAO
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/mol_type="genomic DNA"
/db xref="taxon:32644"
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	Z		REFERENCE 1 AUTHORS Wilson, J.M., Gao, G., Alvira, M.R. and Vandenberghe, L.H. TITLE Adeno-associated virus (aav) clades, sequences, vectors containing same, and uses therefor	JOURNAL Patent: WO 2005033321-A 79 14-APR-2005; The Trustees of the University of Pennsylvania (US) Location/Qualifiers source 12211		ORIGIN Query Match Query Match Best Local Similarity 100.0%; Pred. No. 0; Marches 2209: Conservative 0: Mismatches 0: Indels 0; Gabs 0;	TICCAGATTGGTCGAGACAACCTCTCTGAGGGATTGG 60	61 GAGTGGTGGACTTGAACCTGGAGCCCGAAGCCGAAGCCAAAGCAGAC 61 GAGTGGTGGACTTGAAACCTGGAGCCCCGAAGCCCAAAGCAGAAC 61 GAGTGGTGGAGCTTTGAAACCTGGAGCCCCGAAGCCCAAAGCAAAGCAGAACAAGCAAAAGAAG	121 GACGGCCGGGCTTCGTGCTTCTGCTTCAAAGTACCTTCGACCTTCAACGACTCGACTACAACGACTCGACTTCAACGACTTCGACTTCGACGACTTCGACGACTTCGACGACTTCGACGAACTCGACGGACCTTCGACGACCTTCGACGACCTTCGACGACCTTCGACGACCTTCGACGACCTTCGACGACCTTCGACGACCTTCGACACACAC	QY 181 AAGGGGAGCCCGTCAACGCGGCGCACGACGCGCCTCCGACCACGACAAGGCCTACGAC 240 Db 181 AAGGGGAGCCCGTCAACGCGGCGGCACGCACCACGACCACGACACACCACACACCCCTCCAACGCCTCCAACGCCTCAACGCCTCAACGCCTCAACGCCTAACGACCCAACGACCAACAACACCAACAACAACAACAACA	OY 241 CAGCAGCTCAAAGCGGGTGACAATCCGTACCTGCGGATATAACCACGCCGACGCGGGTTT 300 241 CAGCAGCTCAAAGCGGGTGACCAATCCGTACCTGCGGTATAACCACGCCGAGGTTT 300	Oy 301 CAGGAGCGTCTGCAAGAAGATACGTCTTTGGGGGCAACCTCGGGCGAGCAGTCTTCCAG 360 	Oy 361 GCCAAGAAGGGGGTTCTCGAACCTCTGGGTCTGGTTGAGGAAGGCGCTAAGACGGCTCCT 420	Qy 421 GGAAAGAAACGTCCGCTAGAGCCCACAAACCCAGACTCCTCCTCGGCCATCGC 480 Db 421 GGAAAGAAACGTCCGCTAGAGCCACAAGAGCCAGACTCCTCCTCGGCATCGC 480	Oy 481 AAGACAGGCCAGCAAAAAAAAGACTCAATTTTGGTCAGACTGGCGACTCAGAG 540	541 TCAGTCCCCGATCCACAACCTCCGGAGAACCTCCAGCAACCCCGCTGCTGGGACCT	Db 541 TCAGTCCCGGATCCACAACCTCTCGGAGAACCTCCAGCAACGCCCGGTGCTGTGGGACCT 600 Qy 601 ACTACAATGGCTTCAGGCGGTGGCGCACCAATGGCAGAAATAACGAAGGCGCCGACGGA 660

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781 TCCAGTGCTTCAACGGGGGCCAGCAACGACCACTTCGGCTACAGGCACCCCCTGG 840

1921 AAGAACCCGCCTCCTCAGATCCTCAAAAACACGCCTGTTCCTGCGAATCCTCCGGCG 1980 1921 AAGAACCCGCTCTTCAGATCTCTCAAAAACACGCCTGTTCTTGTTTTTTTT	BD242766 4718 bp DNA linear PAT 17- ION Adeno-associated virus serum type 1 nucleic acid sequence, and host cell containing the same. BD242766 1 GI:33052536 S JP 200529098-A/1. unidentified unidentified unidentified CE 1 (bases 1 to 4718) RS Wilson, J. M. and Xiao, W.	TITLE Adeno-associated virus serum type 1 nucleic acid sequence, vector and host cell containing the same JOURNAL Patent: JP 2002529098-A 1 10-SEP-2002, THE TRUSTEES OF THE UNIVERSITY OF PENNSYLVANIA COMMENT OS AAV-1 PN JP 200252998-A/1 PP 05-SEP-2002 PP 05-NOV-1999 US 60/107114 PI JAMES M WILSON, WEIDONG XIAO PC C12N15/09, A61X31/711, A61X48/00, A61P43/00, C12N1/15, C12N1/19, PC C12N15/10, C12P21/02/A61X35/76, C12N15/00 CC Adeno-associated virus serum type 1 nucleic acid sequence, CC	CC cell containing the same CC cell containing the same FH Key FH CDS (325). (2206) CDS (2223). (4430). FEATURES 1. 4718 COS Location/Qualifiers 1. 4718 Anol_type="qenomic DNA" /db_xref="taxon:32644"	Query Match 100.0%; Score 2209; DB 6; Length 4718; Best Local Similarity 100.0%; Pred. No. 0; Mismatches 0; Indels 0; Gaps 0; Qy 1 ArdGCTGCGATGGTTATCTTCCAGATTGGCTCGAGGACACCTCTTGAGGGCATTGGC 60
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REFERENCE 1 (bases 1 to 4718) AUTHORS Wilson, J.M. and Xiao, W. TITLE Adeno-associated virus servtype 1 nucleic acid sequences, vectors and host cells containing same	· 음 &	GOGTATITICALCACAGATICCACTGCCACTTTICACCACGTGACTGGCACGACTCACTACACAACAACAACAACAACAACAACAACAACAA
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Submitted (05-MAY-1998) IHGT, University of Pennsylvania, 3601
Spruce Street, Philadelphia, PA 19104, USA
Location/Qualifiers
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Viruses; ssDNA viruses; Parvoviridae; Dependovirus. 1
1 (bases 1 to 4718)
Xiao, W., Chirmule, N., Berta, S.C., McCullough, B., Gao, G. and Wilson, J.M.
                                                       TITACCTGGACTGGTGCTTCAAAATATAACCTCAATGGGCGTGAATCCATCATCATCACCT
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Xiao, W. and Wilson, J.M.
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Query Match 99.7%; Score 2202.6; DB 6; Length 7447; Best Local Similarity 99.8%; Pred. No. 0; Matches 2205; Conservative 0; Mismatches 4; Indels 0; Gaps 0; ATGGCTGCGATGGTTATCTTCCAGATTGGTCGAGGACAACCTCCTGAGGGCATTGGC 0	AAGGGGAGCCCTACAACGCGGCGCAGCGGCCCTCCGAGCACGACGCCTACGACAACGCCTACGACAACGCCTACGACAACGCCTACGACAACGCCTACGACAACGCCTACGACAACGCCGCGGCGCCCTCGAGCACGACACAACGCCTACGACACACAC	301 Chodadgearcregehadaracarcregegearcregegegearcrecks 102 Chodadgearcregehadaracarcregegearcregegearcrecks 103 Chodadgearcregehadaracarcrregegearcregegearcrecks 104 Georaga Agegegrateregarcregereregegeargegearcrecks 105 Georaga Agegegrateregarcregeregeregegeargegeregegeregegeregegeregegeregegeregegeregegeregegeregegeregegeregegereg	421 GGAAAGAACGTCCGGTAGACGTCGCCACAAGAGCGACTCCTCCTCCTCGGCATCGGATCGGCATCGGATCGATC	5101 AAGACAGGCCAGCAGCCGGTAAAAAGAGACTCAATTTTGGTCAGACTGGCGACTCAGAG 541 TCAGTCCCCGATCCACAACCTCTCGGAGAACCTCCAGCAACCCCCGGTGCTGTGGGACCT [ACTACAATUGGCTTCAGGGGGGGACCAATGGCAATAACGAAAGACGACGGGACGGAACGGAAGACGAATGAAGAAGACGCCGAACGGAAGACGAATGAAATAACGAATTCGCATTCCACATGGCTTCGACATGGCATCGAATACGCAATGCCAATGCCAATGCCAATGCCAATGCCAATGCCAATGCCAATGCCAATGCCAATGCCAATGCCAATGCCAATGCCAATGCCAATGCCAATGCCAATGCCAATGCAATGCCAATGCCAATGCCAATGCCAATGCCAATGCCAATGCCAATGCCAATGCCAATGCCAATGCCAAGAAATCAATAACCAACC	2311 781 T 5401 T 841 G	Db 5461 dddratrtrgatrtrgadaartccactactactactactacacacacacacacacaca	DD 5581 GTCAAGGAGGACGAACGAATGATGGCGTCACAACCATCGCTAATAACCTTACCAGCACG 5640 Qy 1021 GTTCAAGTCTTCTCGGACTCGGAGTACCAGCACG 1080

	661 GTGGGTAATGCCTCAGGAAATTGGCATTGCGATTCCACATGGCTGGGGGACAAGTCATC 720 661 GTGGGTAATGCCTCAGGAAATTGGCATTGCGATTCCACATGGCTGGGGGACAAGTCATC 720 721 ACCACCAGCACCCGCACCCTGGCCTTGCCATTCCATTACACACCAACCA		102	1021 GTTCAAGTCTTCTGGGACTCGGAGTACCAGCTTCCGTACGTCCTCGGCTCTGGGCACCAG 1080 1081 GGCTGCCTCCCTCCGTTCCCGGCGGAAGTGTTCATGATTCCGCAATACGGCTACCTGACG 1140	CTCAACAATGGCAGCCAAGCCGTGGGACGTTCATCCTTTTACTGCCTGGAATATTTCCCT	1201 TCTCAGATCCTGAGAACGGGCAACTATACCTTCAGCTACACTTTGAGGAAGTGCCT 1280		TIGCTGTTTAGCCGTGGGTCCCAGCTGCCATCTCTGTCGCGTGCCCAAAACTGGCTACCTTTGGCTTTCAGCCCAAAACTGGCTACCTTTGGCTGCTTCTGTTCAGCCCAAAACTGGCTACCTTTGCCGTTTAGCCGTGGGTCTCCTGTTCAGCCCAAAAACTGGCTACCTTTGGCTTTCAGCCCAAAAACTGGCTACCTTTGGCTTTCAGCCCAAAAACTGGCTACCTTTCAGCCCAAAAACTGGCTACCTTTCAGCCCAAAAACTGGCTACCTTTCAGCCCAAAAACTGGCTACCTTTCAGCCCAAAAACTGGCTACCTTTCAGCCCAAAAACTGGCTACCTTTCAGCCCAAAAACTGGCTACCTTTCAGCCCAAAAACTAGCTACCTTTCAGCCCAAAAACTGGCTACCTTTCAGCCCAAAAACTGGCTACCTTTCAGCCCAAAAACTGGCTACCTTTCAGCCCAAAAAACTGGCTACCTTTCAGCCCAAAAAACTGGCTACCTTTCAGCCCAAAAACTGGCTACCTTTCAGCCCAAAAAACTGGCTACCTTTCAGCCCAAAAACTGGCTACCTTTCAGCCCAAAAACTGGCTAGCCAAAAAACTGGCTAGCCTAGCTAG	1411 GGACCCTGTTATCGGCAGCAGCAGCTTTCTAAACAAAAACAAAAACAAAAACAAAAACAAAAAA	TTTACCTGGACTGGTGCTTCAAAATATAACCTCAATGGGGGTGAATCCATCATCAACCCT 1 GGCACTGGTATGGCCTCAAAAAAAAAAGACGAGAAGAAGACAAAGTTCTTTCCCATGAGCGGTGTC 1	GGCACCGCTGTGGCCTCACAAAGACGACGAAGAAATTCTTTCCCATGAGCGGTGTC ATGATTTTTCGAAAAAAGACGCCGGAGCTTCAAACACTGCATTGGACAATGTCATGAAAATTGTAAAAAAAA	AIGAITITIGGAAAAGAGAGCGCCGGAGCTTCAAGCACTGCATTGGACAATGTCATGATT 1
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6721 TACACATCCAATTATGCAAAATCTGCCAACGTTGATTTTACTGTGGACAACAATGGACTT 6780 2161 TATACTGAGCCTCGCCCCATTGGCACCGTTACCTTACCCGTCCCCTGT 2209	RESULT 10 CS073490 CS073490 LOCUS CS073490 CS073490 DEFINITION Sequence 78 from Patent W02005033321. DEFINITION Sequence 78 from Patent W02005033321. DEFINITION Sequence 78 from Patent W02005033321. CS073490.1 GI:63090469 KEYWORDS CS073490.1 GI:63090469 KEYWORDS CS073490.1 GI:63090469 KEYWORDS Unidentified ORGANISM unidentified Unclassified.	REFERENCE 1 AUTHORS Wilson, J.M., Gao, G., Alvira, M.R. and Vandenberghe, L.H. TITLE Adeno-associated virus (aav) clades, sequences, vectors containing same, and uses therefor 500RNAL Patent: WO 20050333121-A 78 14-APR-2005; The Trustees of the University of Pennsylvania (US) FEATURES Location/Qualifiers Antree	2	Gaps TTCGC	1 ATGGCTGCCGATGGTTATCTTCCAGATTGGCTCGAGGACAACCTCTCTGAGGCATTCGC 60 61 GAGTGGTGGGACTTGAAACCTGGAGCCCCAAAGCCCAACCAGCAACGCAAAAGCAGCA 120 61 GAGTGGTGGGACTTGAAACCTGGAGCCCGAAGCCCAAGCCAACCAGCAAAAGCAGGA 120	121 GACGGCCGGGGTCTGGTTCCTGGCTACAAGTACCTCCGACCCTTCAACGGACTCGAC 180 	181 AAGGGGAGCCCGTCAACGCGGCGGCGCCCTCGAGCACGACGACGACGACCTACGAC 240 181 AAGGGGAGCCCGTCAACGCGGCGGACGCGGCGCTCGAGCACGACGACGACGCGC 240 241 CAGCAGCTCAAAGCGGGCGACGCACCCGTCTCGAGCACGCGCGAGCTTT 300	241 CAGCAGCTCAAAGGGGTGACTATTCTGTATTTTTTTTTT	361 GCCAAGAAGCGGGTTCTCGAACCTCTCGGTTGATTGAGAAGGCGCTAAGACGGCTCCT 420 	421 GGAAAGAACGTCCGGTAGAGCACTCGCCACAAGAGCCAGACTCCTCCTCGGGCATCGGC 480 	481 AAGACAGGCAGCAGCAGCTAAAAAGACACTCAATTTTGGTCAGACTGGCGACTCAGAG 540	541 TCAGTCCCGGATCCACAACCTCTCGGAGACCTCCAGCAACCCCCGGTGCTGTGGGACCT 600

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IVI.PGYKYLGPFNGLDKGEPVNAADAAALEHDKAYDOOLKAGDNPYLKYNHADAEYG
RIQBDTSPGGNLGRAV PQAKKRVLEPLGI VEBGAKTRPVEGASPQEBDSBGIG
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NNLTSTVQVFSDSBYQLPYVLGASANGOCLPPPRADVFMI PQYGYLTLNNGSQAVGRSS
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NQSGSAQNKDLLFSRGSPAGMSVQPKNMLPQPCYRQORVSKTKTDNNNSNFTWTGASK
YNLNGRESI INPGTRAVSSHKDDEDKFPPMSGVMI FGKRSAGASSTALDNWNTTDEEEI
KATNPVATERFGTVAVNFGSSSTDPATGDVAMGALPGMVMODRDVYLQGPI MAKI PH
TDGHIFHPSPLMGGFGLKNPPPQI LIKNTPVPANPARESSATKRASFITGYSTGVSVE
I EWELQKENSKRWNPEVQYTSNYAKSANVDPTVDNNGLYTEPRPIGTRYLTRPL"
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                                                                    product="capsid protein VP1"
fprotein_id="AAS99296.1"
/db_xref="G1:46487869"
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Pred. No. 0;
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/gene="cap"
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1 (bases i to 2211)
2006, Vandenberghe, L. H., Alvira, M.R., Lu, Y., Calcedo, R., Zhou, X. and Wilson, J.M.
Clades of Adeno-associated viruses are widely disseminated in human
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2 (bases 1 to 2211)

and Wilson,J.M.

and Milson,J.M.

Direct Submission

Submitted (20-JAN-2004) Gene Therapy Program, Division of Medical
Genetics, Department of Medicine, University of Pennsylvania, 3601

Spruce Street, Mistar Institute, Philadelphia, PA 19104, USA

Location/Qualifiers
                                                                                                                                                                                                                                                              1861 AAAATTCCTCACACAGATGGACACTTTCACCCGTCTCCTCTTATGGGCGGCTTTGTGGACTC
                                      1681 ACAGACGAAAAGAGGAAATTAAAGCCACTAACCCTGTGGCCACCGAAAGATTTGGGACCGTG
                                                                                                              1741 GCAGTCAATTTCCAGAGCAGCAGCACCAGCGACCGGAGATGTGCATGCTATGGGA
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Organism="Adeno-associated virus"
(mol type="genomic DNA"
/isolate="hu.48"
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/db_xref="taxon:272636"
/country="USA"
/note="clade A"
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        GCCAAGAAGCGGGTTCTCGAACCTCTCGGTCTGGTTGAGGAAGCTGCTAAGACGGCTCCT
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                                                           GGAAAGAAACGTCCGGTAGAGCAGTCGCCACA---AGAGCCAGACTCCTCCTCGGGCATC
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and Wilson, J.W.
Clades of Adeno-associated viruses are widely disseminated in human tissues
J. Virol. 78 (12), 6381-6388 (2004)
ED 5153731
CE 2 (bases 1 to 2214)
Gao.G., Vandemberghe, L.H., Alvira, M.R., Lu,Y., Calcedo,R., Zhou,X.
Rand Wilson,J.W.
Direct Submission
AL Submitsed (20-JAN-2004) Gene Therapy Program, Division of Medical
Genetics, Department of Medicine, University of Pennsylvania, 3601
Spruce Street, Wistar Institute, Philadelphia, PA 19104, USA
1. Catalon/Qualifiers
1. Catalon/Qualifiers
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Amol_rype="genomic DNA"
/ isolation Bource="human tissue"
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HTDGHFHPSPLMGGFGLKNPPPQILIKNTPVPANPPAEFSATKFASFITQYSTGQVSV
EIEWELQKENSKRMNPEVQYTSNYAKSASVDFTVDNNGLYTEPRPIGTRYLTRPL"
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.larity 97.8%; Pred. No. 0;
Conservative 0; Mismatches 45; Indels 3;
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Matches 2164; Conserv
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ORIGIN Query Match Best Local Similarity 97.2%; Pred. No. 0; Matches 2147; Conservative 0; Mismatches 62; Indels 0; Gaps 0;	GATGGTTATCTTCCAGATTGGCTCGAGGACAACCTCTCTGAGG 	OY 61 GAGTIGGACTTGAAACCTGGAGCCCCGAAGCCCAAAGCCAAAAGCAGGAC 120	9y 121 GACGGCGGGGTTCTGGTACTACAAGTACCTCGGACCCTTCAACGGACTCGAC 180	QY 181 AAGGGGGGCCCTCAACGCGGCCGACGCCCTCGACCACGACGCCTACGAC 240 Db 181 AAGGGAGGCCGGTCAACGAGCGCCCCCCGAGCACGACAAAGCCTACGAC 240	Qy 241 CAGCAGCTCAAAGCQGTGACAATCCGTACCTGCGGTATAACCACGCCGACGCCGACGTTT 300 bb 241 CGGCAGCTCGACGAGACAACCCGTACCTCAAGTACAACCACGCCGACGCGAGGTTT 300	9y 301 CAGGAGCGTCTGCAAGAAGATACGTCTTTTGGGGGGAACCTCGGGCGAGCAACCTTCCAG 360	9y 361 GCCAAGAAGCGGGTTCTCGAACCTCTCGGTCTGAGGAAGCGGCTAAGACGGCTCCT 420	Oy 421 GGAAAGAAACGTCCGGTAGAGCAGTCGCCACAAGAGCCAGACTCCTCTCGGGCATCGGC 480 Db 421 GGAAAGATCGGGTAGAGCACCCCACAAGGCCAGACTCCTCTCGGGCATCGGC 480	Oy 481 AAGACAGCCAGCAGCCGCTAAAAAGAGACTCAATTTTGGTCAGACTGGCGACTCAGAG 540	Oy 541 TCAGTCCCCGATCCACACCTCTCGGAGAACCTCCAGCAACCCCCGCTGTGGGACCT 600 Db 541 TCAGTCCCCGATCCACAACCTCTCGGAGAACCTCCAGCAACCCCCGCTGCTGTGGGACCT 600	0y 601 ACTACAATGGCTTCAGGCGCACCAATGGCAGACAATAACGAAGGCGCCGACGA 660		781 TCCAGTGCTTCAACGGGGCCAGCAACGACAACCACTACTTCGGCTACAGCACCCCTGG 	Qy 841 GGTATTTTGATTTTCAACAGATTCCACTGCCACTTTTCACCAGTGACTGGCAGTC 900 Db 841 GGGTATTTTGATTTCAACAGATTCCACTGCCACTTTTTCACCACGTGACTGGCAGCGACTC 900	QY 901 ATCAACAACAATTGGGGATTCCGGCCCAAGAGACTCAACTTCAACTCTACAACATCCAA 960 Db 901 ATCAACAATTGGGGATTCCGGCCCAAGAGACTCAACTTCAACTTCAACTTCAACATCAA 960	Oy 961 GTCAAGGAGGTCACGACGAATGATGGCGTCACAACCATCGCTAATAACCTTACCAGCACG 1020
Db	Qy 1558 CCTGGCACTGCTATGGCCTCACAAAGACGACGAAGACACATCTTTCCCATGAGCGGT 1617 bb 1561 CCTGGCACTGCTATGGCCTCACACAAAGACGAAGACAAGTTCTTTCCCATGAGCGGT 1620	Qy 1618 GTCATGATTTTGGAAAAGAGGGCCGGAGCTTCAAACACTGCATTGGACAATGTCATG 1677	Qy 1678 ATTACAGAGGAAGAAATTAAAGCCACTAACCCTGTGGCCACCGAAAGATTTGGGACC 1737	Qy 1738 GTGGCAGTCAATTTCCAGAGCAGCACAGACCCTGCGACCGGAGATGTGCATGCTATG 1797	Qy 1798 GGAGCATTACCTGGCATGGCAAGATAGAGACGTGTACCTGCAGGGTCCCATTTGG 1857 Db 1801 GGAGCATTACCTGGCATGGTGGCAAGATAGAGACGTGTACCTGCAGGGTCCCATTTGG 1860	Qy 1858 GCCAAAATTCCTCACACAATGGACATTCACCCGTCTCCTTATGGGCGGCTTTGGA 1917	Qy 1918 CTCAAGAACCCGCCTCCTCAGATCCTCATCAAAAACACGCCTGTTCCTGCGAATCCTCCG 1977	Qy 1978 GCGGAGTTTTCAGCTACAAAGTTTGCTTCATCACCCCAATACTCCCACAGGACAAGTG 2037	Qy 2038 AGTGTGGAAATTGAATGGGAGCTGCAGAAACAAAACAGCAAGCGCTGGAATCCCGAAGTG 2097	Qy 2098 CAGTACACATCCAATTATGCAAAATCTGCCAACGTTGATTTTACTGTGGACAACAATGGA 2157 Db 2101 CAGTACACATCCAATTATGCAAAATCTGCCAGCGTTGATTTTACTGTGGACAACAATGGA 2160	Qy 2158 CTTTATACTGAGCCTCGCCCATTGGCACCGGTTACCTTACCCTGT 2209	RESULT 14 CS073493 CS073493 2211 bp DNA linear PAT 05-MAY-2005 DEFINITION Sequence 81 from Patent W02005033321. VERSTON CS073493 1 GT.63090472	_	REFERENCE 1 AUTHORS Wilson, J.M., Gao, G., Alvira, M.R. and Vandenberghe, L.H. TITLE Adeno-associated virus (aav) clades, sequences, vectors containing same, and uses therefor	DOUGNAL FATERI: MC ZUDO3331-A B1 14-AFK-ZUD3; FEATURES The Trustees of the University of Pennsylvania (US) SOURCE 12211	/organism="unidentified" /mol_type="unassigned DNA" /db_xref="taxon132644" /noTe="new AAV serotype, clone hu.44"

Search completed: November 29, 2005, 00:05:32 Job time : 8078.36 secs

(OTARU) XXXXXIII BAAA SIHT

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Geguence 1, Application US/09807802A
; Patent No. 6759237
; GENERAL INFORMATION:
APPLICANT: Wilson, James M.
; APPLICANT: Xiao, Weidong
; TITLE OF INVENTION: Adeno-Associated Virus Serotype I Nucleic Acid Sequences,
TITLE OF INVENTION: Vectors and Host Cells Containing Same
; TITLE OF INVENTION: Vectors and Host Cells Containing Same
; TITLE OF INVENTION: Vectors and Host Cells Containing Same
; TITLE OF INVENTION: Vectors and Host Cells Containing Same
; TITLE OF INVENTION: Vectors and Host Cells Containing Same
; FILE REFERENCE: 2002-02-21
; PRIOR PPLICATION NUMBER: US 60/107,114
; PRIOR FILING DATE: 1998-11-05
; PRIOR FILING DATE: 1999-11-02
; NUMBER OF SEQ ID NOS: 20
; NUMBER OF SEQ ID NOS: 20
; NUMBER PATENTALE: PATENTIN Version 3.1
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Sequence 7, Appli
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Similarity 100.0%; Pred. No. 2.7e-30;
13; Conservative 0; Mismatches 0;
US-09-299-141-4
US-09-299-141-8
US-09-299-141-8
US-08-299-141-8
US-08-893-327-15
US-08-893-327-17
US-08-893-327-19
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US-09-299-141-10
US-09-299-141-11
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US-09-807-802A-1
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OTHER INFORMATION:
     ORGANISM: AAV-1
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Matches 143; C
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LENGTH: 4718
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/cgn2_6/ptodata/1/ina/6_COMB.seq:*
/cgn2_6/ptodata/1/ina/H_COMB.seq:*
/cgn2_6/ptodata/1/ina/PCTUS_COMB.seq:*
/cgn2_6/ptodata/1/ina/PCTUS_COMB.seq:*
/cgn2_6/ptodata/1/ina/PCTUS_COMB.seq:*
/cgn2_6/ptodata/1/ina/PCTUS_COMB.seq:*
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(c) 1993 - 2005 Compugen Ltd.
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Listing first 45 summaries
                                                                                                                                   - nucleic search, using sw model
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Gapop 10.0 , Gapext 1.0
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Maximum DB seq length: 200000000
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                                    Score 119; DB 3; Length 4718; Pred. No. 1.1e-23; 0; Mismatches 15; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 1, Application US/07789917A
Fatent No. 552479
GENERAL INFORMATION:
APPLICANT: Stivestave, Arun
TITLE OF INVENTION: SAPE VECTOR FOR GENE THERAPY
NUMBER OF SEQUENCES: 2
CORRESPONDENCE ADDRESS:
ADDRESSE: Scully, Scott, Murphy Presser
STREET: 400 Garden City Plaza
CTTY: Garden City
STATE: New York
COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM FO Compatible
COMPUTER: TBM FO Compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release q.0, Version q.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07/789,917A
FILING DATE: 19911118
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: MCMULLY, William E.
REGISTRATION NUMBER: 2.5,606
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Score 107.4; DB 2;
Pred. No. 1.2e-20;
0; Mismatches 21;
                                                                                                                                                                                                                                                                                                                                    1598 GGCAACTCCATCACTAGGGGTAA 4576
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TELECOMUNICATION INFORMATION:
TELEPHONE: (516) 742-4343
TELEFA: 230 901 SANS UR
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 145 base pairs
                                         83.2%;
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ilarity 85.1%;
Conservative
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TYPE: NUCLEIC ACID
STRANDEDNESS: single
                                                            Best Local Similarity 89.5
Matches 128; Conservative
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Best Local Similarity
Matches 120; Conserv
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US-07-789-917A-1
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US-09-807-802A-1
                                           Query Match
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                                                                         Sequence 19, Application US/09807802A

Patent No. 6755237

GENERAL INFORMATION:
APPLICANT: Xiao, Weidong
TITLE OF INVENTION: Vectors and Host Cells Containing Same
TITLE OF INVENTION: Vectors and Host Cells Containing Same
TITLE OF INVENTION: Vectors and Host Cells Containing Same
TITLE OF INVENTION: Vectors and Host Cells Containing Same
CURRENT APPLICATION NUMBER: US/09/807,802A

CURRENT APPLICATION NUMBER: US/09/807,802A

PRIOR PILING DATE: 1998-11-05

PRIOR PILING DATE: 1998-11-05

NUMBER OF SEQ. ID NOS: 20

SOFTWARE: Patentin version 3.1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 1, Application US/09807802A

Sequence 1, Application US/09807802A

Patent No. 675937

GENERAL INFORMATION

APPLICANT: Wilson, James M.

APPLICANT: Xiao, Weddong

TITLE OF INVENTION: Vectors and Host Cells Containing Same

TITLE OF INVENTION: Vectors and Host Cells Containing Same

FILE REFERENCE: GNVPN 03103A

CURRENT APPLICATION NUMBER: US/09/807,802A

CURRENT PEDIAGATION NUMBER: US 60/107,114

PRIOR FILING DATE: 1998-11-05

PRIOR FILING DATE: 1999-11-02

NUMBER OF SEQ ID NOS: 20
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Pred. No. 1.1e-28;
0; Mismatches 3;
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SEQ ID NO 1
LENGTH: 4718
TYPE: DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match
Best Local Similarity 97.9%;
Matches 139; Conservative
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LOCATION: (2223)..(4430)
OTHER INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         LOCATION: (335)...(OTHER INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ORGANISM: AAV-6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ORGANISM: AAV-1
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US-09-807-802A-1/c
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85.1%; Pred. No. 1.2e-20;
wismatches 21; Indels
                                                                                                                     Sequence 1, Application US/07982193

Patent No. 6261834

GENERAL INFORMATION:
GENERAL INFORMATION:
TITLE OF INVENTION: SAFE VECTOR FOR GENE THERAPY
NUMBER OF SEQUENCES: 2
CORRESPONDENCE ADDRESS:
ADDRESSEE: Scully, Scott, Murphy & Presser
STREET: 400 Garden City Plaza
CITY: Garden City
STATE: New York
COUNTRY: USA
ZIP: 11530
COMPUTER: Floppy disk
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
COMPUTER: IBM PC compatible
COMPUTER: IBM PC compatible
COMPUTER: IBM PC compatible
COMPUTER: 19921125
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07/982,193
FILING DATE: 19921125
CLASSIFICATION HOMBER: 22,666
REGISTRATION NUMBER: 22,666
REGISTRATION NUMBER: 22,666
REGISTRATION NUMBER: 22,666
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Patent No. 6916635
GENERAL INFORMATION:
APPLICANT: Hearing, Patrick
APPLICANT: Bahou, Wadie
APPLICANT: Bandalon, Ziv
TITLE OF INVENTION: Adenoviral Vectors
FILE REFERENCE: STONYBR-0490;
CURRENT APPLICATION DAILE: 2001-02-12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  121 GGCAACTCCATCACTAGGGGT 141
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NAME: NUMBER: LANGER REGISTRATION NUMBER: LANGERER REFERENCE/DOCKET NUMBER: 8361
TELECOMMUNICATION INPORMATION:
TELEPRONE: (516) 742-4343
TELEX: 230 901 SANS UR
INPORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 145 base pairs
TYPE: NUCLEIC ACID
TYPE: NUCLEIC ACID
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US-07-982-193-1
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Matches 120; Conservative
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US-09-782-378A-6
                                                                    RESULT 6
US-07-982-193-1
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                                                                                                                                                                                                         Sequence 4, Application US/08702573
Patent No. 6033885
CENERAL INFORMATION:
CENERAL INFORMATION:
CENERAL LATTA, Martine
APPLICANT: DENEFLE, Patrice
APPLICANT: USINE Emmanuelle
APPLICANT: VIGNE, Emmanuelle
APPLICANT: VIGNE, Emmanuelle
APPLICANT: VIGNE, Martine
APPLICANT: VIGNE, PREPARATION THEREOF AND THERAPEUTICAL USES THEREOF NUMBER OF SEQUENCES: 13
CORRESPONDENCE ADDRESS:
ADDRESSEE: Rhone-Poulenc Rorer Inc.
STREET: 500 Arcola Rd. 3C43
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            0; Gaps
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LOCATION: 1..145
OTHER INFORMATION: /note= "Minimal ITR Sequence"
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ZIP: 19426

MEDIUM TYRER READABLE FORM:
MEDIUM TYRE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/NS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30

CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/702,573
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CLASSIFICATION: 424
PRIOR APPLICATION DATA;
APPLICATION NUMBER: FR 94/02445
FILING DATE: 03-MAR-1994
PRIOR APPLICATION NUMBER: FR 94/02445
FILING DATE: 28-FEB-1995
ATTORNEY AGENT INFORMATION:
NAME: Smith Ph.D., Julie K.
REGISTRATION NUMBER: 38,619
FEFERENCE/DOCKET NUMBER: ST94011-US
TELEPHONE: (610)454-3839
TELEPHONE: (610)454-3839
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121 GCCAACTCCATCACTAGGGGT 141
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TYPE: nucleic acid
STRANDEDNESS: double
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INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
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USA
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Gaps

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Length 145;

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MOLECULE TYPE: DNA (genomic)
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                                                                                                                                                                                              Length 145;
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"Gequence 1, Application US/07989841A

"Bequence 1, Application US/07989841A

"APPLICANT: Samulaki, R. J.

APPLICANT: Xiao, X.

TITLE OF INVENTION:

NUMBER OF SEQUENCES: 6

CORRESPONDENCE ADDRESS:

COTY: New York

CITY: New York

COUNTRY: New York

COUNTRY: U.S.A.

ZIP: 10036-271

COMPUTER READALE FORM:

MEDIUM TYPE: Floppy disk

COUNTRY: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: PatentIn Release #1.0, Version #1.25

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/07/989,841A

FILING DATE: On even date herewith

CLASSIFICATION NUMBER: 30,742

REGISTRATION NUMBER: 30,741

TELEPHONE: (212) 790-9090

TELEPHONE: (212) 790-9090

TELEPHONE: (212) 790-9090

TELEPHONE: GIAL PERNIE

INFORMATION FOR SEQ ID NO: 1:

SEQUENCE CHARACTERSTICS:

LENTH: 155 base pairs

TYPE: nucleic acid

STRANDEDNESS: double
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Indels
                                                                                                                                                                                            Query Match
75.1%; Score 107.4; DB 3;
Best Local Similarity 85.1%; Pred. No. 1.2e-20;
Matches 120; Conservative 0; Mismatches 21;
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PRIOR APPLICATION NUMBER: 60/237,747
PRIOR FILING DATE: 2000-10-02
NUMBER OF SEQ ID NOS: 27
SOFTWARE: PATENTIN VERSION 3.0
SEQ ID NO 6
LENGTH: 145
                                                                                                                                                                                                                                                                                                                                                                                                                             GGCAACTCCATCACTAGGGGT 141
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MOLECULE TYPE: DNA (genomic)
                                                                                                                 TYPE: DNA
CNGANISM: Homo sapiens
US-09-782-378A-6
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21 Tradeceacrectereraegecreereeres 80
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                                                                                                                                                                                                                                                                                                                                                                                    APPLICANT: Samulaki, R. J.
APPLICANT: Samulaki, R. J.
APPLICANT: Xiao, X.
IITLE OF INVENTION: Recombinant Viral Vector System
NUMBER OF SEQUENCES: 6
CORRESPONDENCE ADDRESS:
ADDRESSEE: Pennie & Edmonds
STREET: 1155 Avenue of the Americas
CITY: New York
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              STATE: New York
COUNTRY: U.S.A.
ZIP: 10036-2711
COMPUTER: READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: Ploppy disk
COMPUTER: Ploppy disk
COMPUTER: Parent Floppy disk
COMPUTER: Parent Floppy disk
COMPUTER: Parent Floppy disk
SOFTWARE: Parent Floppy DATA:
APPLICATION NUMBER: US/08/440,738A
FILING DATE: May 15, 1995
CLASSIFICATION: 435
CLASSIFICATION: 435
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                                                                                                                                                                                                                                                                  RESULT 9
US-08-440-738A-1
; Sequence 1, Application US/08440738A
; Patent No. 586905
; Patent INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ATTORNEY AGENT INFORMATION:
NAME: Coruzzi, Laura A
REGISTRATION UNDER: 30,742
REFERENCE/DOCKET NUMBER: 6636-(
TELECOMMUNICATION INFORMATION:
TELEFAX: (212) 790-9090
TELEX. 66141 PENNIE
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 165 base pairs
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y Sequence 8, Application US/09782378A
Fatent No. 691635
GENERAL INFORMATION:
APPLICANT: Bearing, Patrick
APPLICANT: Bahou, Wadie
APPLICANT: Bahou, Wadie
TITLE OF INVENTION: Adenoviral Vectors
FILE REFERENCE: STOWNS-04907
CURRENT APPLICATION NUMBER: US/09/782,378A
CURRENT FILING DATE: 2001-02-12
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SOTTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 7
LENGTH: 165
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PRIOR FILING DATE: 2000-10-02
NUMBER OF SEQ ID NOS: 27
SOFTWARE: PatentIn version 3.0
                                                                                                                              121 GGCAACTCCATCACTAGGGGT 141
                                                                                                                                                                                             141 GCCAACTCCATCACTAGGGGT 161
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Best Local Similarity 85.1%;
Matches 120; Conservative
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US-09-782-378A-8
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      US-10-054-665A-7
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; OTHER INFORMATION: SEQ ID NO:1 of U.S. Patent No. 6436392 5,478,745
US-09-276-625-7
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85.1%; Pred. No. 1.2e-20;
ive 0; Mismatches 21; Indels
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Pred. No. 1.2e-20;
0; Mismatches 21; Indels
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APPLICANT: Duan, Dongsheng
TITLE OF INVENTION: Adeno-associated virus vectors
FILE REPERENCE: 875.007031
CURRENT APPLICATION NUMBER: US/09/276,625
CURRENT RILING DATE: 1999-03-25
PRIOR APPLICATION NUMBER: US 60/086,166
PRIOR APPLICATION NUMBER: 1399-05-20
NUMBER OF SEQ ID NOS: 13
SOPTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 7
SEQ IN NO 7

                                                                                                                                                                                       GENERAL INFORMATION:
APPLICANT: Samulaki, R.
APPLICANT: Samulaki, R.
TITLE OF INTENTION: RECOMBINANT VIRAL VECTOR SYSTEM
FILE OF INTENTION: RECOMBINANT VIRAL VECTOR SYSTEM
FILE REFERENCE: 6636-027
CURRENT APPLICATION NUMBER: US/08/471,914A
CURRENT FILING DATE: 1995-06-06
EARLIER PILING DATE: 1995-05-15
NUMBER OF SEQ ID NOS: 13
SOFTWARE: PATENTIN Ver. 2.0
SEQ ID NO 1
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                                                                     Sequence 1, Application US/08471914A
Patent No. 6057152
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TYPE: DNA ORGANISM: Artificial Sequence
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Best Local Similarity 85.1%;
Matches 120; Conservative
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Best Local Similarity 85.1<sup>1</sup>
Matches 120; Conservative
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Pred. No. 1.2e-20;
0; Mismatches 21; Indels 0
Sequence 7, Application US/10054665A

Sequence 7, Application US/10054665A

GENERAL INFORMATION:
APPLICANT: Engelhardt, John F.
APPLICANT: Duan, Dongshen
TITLE OF INVENTION: Adeno-associated virus vectors
FILE REFERENCE: 875.007US2
CURRENT APPLICATION NUMBER: US/10/054,665A
CURRENT FILING DATE: 1998-05-20
PRIOR FILING DATE: 1998-05-20
PRIOR FILING DATE: 1999-03-25

PRIOR RELIGING DATE: 1999-03-25

PRIOR RELIGING DATE: 1999-03-25
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   DB 3; Length 165;
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                                       Indels
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APPLICANT: Duan, Dongsheng
TITLE OF INVENTION: Adeno-associated virus vectors
FILE REFERENCE: 875.0070S1
CURRENT APPLICATION NUMBER: US/09/276,625
CURRENT FILING DATE: 1999-03-25
PRIOR APPLICATION NUMBER: US 60/086,166
PRIOR APPLICATION NUMBER: 1998-05-20
NUMBER OF SEQ ID NOS: 13
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 6
LENGTH: 272
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Patent No. 6897045
GENERAL INFORMATION:
APPLICANT: Engelhardt, John F.
APPLICANT: Duan, Dongshen
APPLICANT: Duan, Dongshen
TILLE OF INVENTION: Adeno-associated virus vectors
FILE REFERENCE: 875.007032
CURRENT FILING DATE: 2002-01-22
PRIOR PILICATION NUMBER: US 60/086,166
PRIOR FILING DATE: 1998-05-20
PRIOR PILING DATE: 1998-05-20
PRIOR FILING DATE: 1999-03-25
NUMBER OF SEQ ID NOS: 14
SOFTWARE: FastSEQ for Windows Version 4.0
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 Score 107.4; DB 3;
Pred. No. 1.2e-20;
0; Mismatches 21;
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ORGANISM: AAV circular intermediate, clone p1202
US-09-276-625-6
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Patent No. 6436392
GENERAL INFORMATION:
Query Match
Best Local Similarity 85.1%;
Matches 120; Conservative
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US-10-054-665A-6
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US-09-276-625-6
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Best Local Similarity 85.1%; Pred. No. 1.2e-20;
Matches 120; Conservative 0; Mismatches 21; Indels
            LENGTH: 272
TYPE: DNA
ORGANISM: AAV circular intermediate, clone p1202
US-10-054-665A-6
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; Sequence 1, Application US/09807802A
; Batent No. 675937
; GENERAL INFORMATION:
APPLICANT: Wilson, James M.
APPLICANT: Xiao, Weidong
TITLE OF INVENTION: Adeno-Associated Virus Serotype I Nucleic Acid Sequences,
TITLE OF INVENTION: Vectors and Host Cells Containing Same
TITLE OF INVENTION: Vectors and Host Cells Containing Same
FILE REFERENCE: GNVPN. 031USA
; TITLE OF INVENTION: Vectors and Host Cells Containing Same
; FILE REFERENCE: 2002-02-21
; PRIOR APPLICATION NUMBER: US 60/107,114
; PRIOR APPLICATION NUMBER: PCT/US99/25694
; PRIOR PLING DATE: 1998-11-02
; PRIOR FILING DATE: 1999-11-02
; NUMBER OF SEC ID NOS: 20
; SOFTWARE: Patentin version 3.1
; SEC ID NOS: 20
; FEWALL SEC ID NOS: 20
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Sequence 1,
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Sequence 1,
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llarity 100.0%; Pred. No. 2.2e-30;
Conservative 0; Mismatches 0;
US-09-394-110A-1

US-09-276-625-6

US-09-394-110A-2

US-07-789-917A-1

US-07-989-917A-1

US-09-702-573-4

US-09-702-573-4

US-09-702-573-4

US-09-702-573-4

US-09-702-573-4

US-09-702-573-4

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      , LUCATION: (2223)..(4430); OTHER INFORMATION:
US-09-807-802A-1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NAME/KEY: CDS
LOCATION: (335)..(2206)
OTHER INFORMATION:
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Best Local Similarity
Matches 143; Conserv
          ORGANISM: AAV-1
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                                                                                                                                                                                                                                            November 28, 2005, 19:15:02 ; Search time 20.3389 Seconds (without alignments) 12497.813 Million cell updates/sec
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/cgn2_6/ptodata/1/ina/6A_COMB.seq:*
/cgn2_6/ptodata/1/ina/6B_COMB.seq:*
/cgn2_6/ptodata/1/ina/H_COMB.seq:*
/cgn2_6/ptodata/1/ina/PCOMB.seq:*
/cgn2_6/ptodata/1/ina/PCOMB.seq:*
/cgn2_6/ptodata/1/ina/PCOMB.seq:*
/cgn2_6/ptodata/1/ina/PCOMB.seq:*
/cgn2_6/ptodata/1/ina/RE_COMB.seq:*
/cgn2_6/ptodata/1/ina/RE_COMB.seq:*
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(c) 1993 - 2005 Compugen Ltd.
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US-09-807-802A-19
US-09-807-802A-18
US-08-525-866-1
US-08-440-738A-1
US-08-441-914-1
US-08-471-914-1
US-08-471-914-1
US-08-78-573-3
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US-09-276-625-4
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Maximum Match 100%
Listing first 45 summaries
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; TYPE: DNA
; ORGANISM: AAV-6
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US-09-807-802A-1
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Sequence 1, Application US/09807802A

Sequence 1, Application US/09807802A

Sequence 1, Application US/09807802A

GENERAL INPERMATION.

APPLICANT: Xiao, Weidong

TITLE OF INVENTION: Adeno-Associated Virus Serotype I Nucleic Acid Sequences,

TITLE OF INVENTION: Adeno-Associated Virus Serotype I Nucleic Acid Sequences,

TITLE OF INVENTION: Adeno-Associated Virus Serotype I Nucleic Acid Sequences,

CURRENT APPLICATION WUMBER: US/09/807,802A

CURRENT FILING DATE: 1998-11-05

PRIOR FILING DATE: 1998-11-05

NUMBER OF SEQ ID NOS: 20

SOFTWARE: Patentin version 3.1

SEQ ID NO 1

LENTH: 4718
                                                                                                                                APPLICANT: Mison, James M.
APPLICANT: Xiso, Weldong
TITLE OF INVENTION: Adeno-Associated Virus Serotype I Nucleic Acid Sequences,
TITLE OF INVENTION: Adeno-Associated Virus Serotype I Nucleic Acid Sequences,
TITLE OF INVENTION: Vectors and Host Cells Containing Same
FILE REFERENCE: GNVPN.031USA
CURRENT APPLICATION NUMBER: US/09/807,802A
CURRENT APPLICATION NUMBER: US 60/107,114
PRIOR FILING DATE: 1998-11-05
PRIOR FILING DATE: 1999-11-02
NUMBER OF SEQ ID NOS: 20
SOFTWARE: PATENTIN VERSION 3.1
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Pred. No. 4.3e-24;
0; Mismatches 3;
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                                                                         Sequence 19, Application US/09807802A
Patent No. 6759237
GENERAL INFORMATION:
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Best Local Similarity 97.6%;
Matches 122; Conservative
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LOCATION: (2223)..(4430)
OTHER INFORMATION:
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ORGANISM: AAV-1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    US-09-807-802A-19
                                                                                                                                                                                                                                                                                                                                                                                                      SEQ ID NO 19
LENGTH: 4683
                                                                                                                                                                                                                                                                                                                                                                                                                                                TYPE: DNA
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US-09-807-802A-19
| Sequence 19, Application US/09807802A
| Sequence 19, Application US/09807802A
| Petent No. 6759237
| GENERAL INFORMATION:
| APPLICANT: Wilson, James M. APPLICANT: Wilson, James M. APPLICANT: Wilson, James M. TITLE OF INVENTION: Methon-Associated Virus Serotype I Nucleic Acid Sequences, TITLE OF INVENTION: Vectors and Host Cells Containing Same
| TITLE OF INVENTION: Vectors and Host Cells Containing Same
| TITLE OF INVENTION: Vectors and Host Cells Containing Same
| TITLE OF INVENTION: Vectors and Host Cells Containing Same
| CURRENT APPLICATION NUMBER: US/09/807,802A
| CURRENT FILING DATE: 1998-11-02
| PRIOR FILING DATE: 1998-11-02
| PRIOR FILING DATE: 1998-11-02
| NUMBER OF SEQ ID NOS: 20
| SOFTMARKE: Patentin Version 3.1
| SEQ ID NO 199
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US-09-807-802A-18
Sequence 18, Application US/09807802A
Factor of 579237
GENERAL INFORMATION:
APPLICANT: Wilson, James M.
APPLICANT: Xiao, Weldong
TITLE OF INVENTION: Vectors and Host Cells Containing Same
FILE REFERENCE: GNVPN.031USA
CURRENT APPLICATION WHBER: US/09/807,802A
CURRENT PILING DATE: 2002-02-21
PRIOR APPLICATION NUMBER: US 60/107,114
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83.2%; Score 119; DB 3; Length 4718; 89.5%; Pred. No. 9.1e-24; rive. 0; Mismatches 15; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match 79.2%; Score 113.2; DB 3; Length 'Best Local Similarity 87.3%; Pred. No. 3.6e-22; Matches 124; Conservative 0; Mismatches 18; Indels
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                                                         Matches 128; Conservative
     Query Match
Best Local Similarity
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65 GCGACCAAAGGTCGCCCGACGCCCGGGCTTTGCCCGGGCGGCCTCAGTGAGCGAGGAGCAGC 124
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                                           Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CITY: New YORK
COUNTRY: U.S.A.
ZIP: 10036-2711
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07/989,841A
FILING DATE: On even date herewith
FILING DATE: OF even date
FILING DATE: OF even
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 1, Application US/07989841A
Patent No. 5478745
GENERAL INFORMATION:
APPLICANT: Xiao, X.
TITLE OF INVENTION: Recombinant Viral Vector System
NUMBER OF SEQUENCES: 6
CORRESPONDENCE ADDRESS:
ADDRESSEE: Pennie & Edmonds
STREET: 1155 Avenue of the Americas
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       123 GCGCAGAGAGGGAGTGGGCAA 143
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MOLECULE TYPE: DNA (genomic)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match
Best Local Similarity 85.1%;
Matches 120; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CITY: New York
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               US-07-989-841A-1
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US-07-989-841A-1
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                                                                                                                                                                                                                                                                                                                                                                                                                           76.2%; Score 109; DB 3; Length 4681;
85.8%; Pred. No. 5.2e-21;
tive 0; Mismatches 20; Indels (
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           GENERAL INFORMATION:
APPLICANT: NATSOULIS, GEORGES
APPLICANT: PUROSKY, RICHARD T.
TITLE OF INVENTION: TARGETED NUCLEOTIDE SEQUENCE DELIVERY
TITLE OF INVENTION: AND INTEGRATION SYSTEM
NUMBER OF SEQUENCES:
CORRESPONDENCE ADDRESS:
ADDRESSER: REED & ROBINS
STREET: 285 Hamilton Avenue, Suite 200
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Indels
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MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

COMPUTER: IBM PC compatible

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: PatentIn Release #1.0, Version #1.30

CURRENT APPLICATION DATE:

APPLICATION NUMBER: US/08/525,866

FILING DATE: 08-SEP-1995

CLASSIFICATION: 514

ATTORNEY/AGBWT INFORMATION:

NAME: ROBINS, ROBERTA L.

REFERENCE/DOCKET NUMBER: 0800-0006

TELECOMMUNICATION INFORMATION:

TELECOMMUNICATION INFORMATI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match 75.1%; Score 107.4; DB 3; Best Local Similarity 85.1%; Pred. No. 9.9e-21; Matches 120; Conservative 0; Mismatches 21;
                                   PRIOR APPLICATION NUMBER: PCT/US99/25694
PRIOR FILING DATE: 1999-11-02
NUMBER OF SEQ ID NOS: 20
SOFTWARE: Patentin version 3.1
SEQ ID NO 18
LENGTH: 4681
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1661 GCGCAGAGAGGGAGTGGGCAA 4681
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Patent No. 6207457
       PRIOR FILING DATE: 1998-11-05
                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match 76.2
Best Local Similarity 85.8
Matches 121; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           STREET: 285 Hami.
CITY: Palo Alto
STATE: CA
COUNTRY: USA
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                                                                                                                                                                                                                                                                       TYPE: DNA
ORGANISM: AAV-2
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                                                                                FEATURE:
OTHER INFORMATION: Description of Artificial Sequence: double-D
OTHER INFORMATION: sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match 75.1%; Score 107.4; DB 3; Length 165; Best Local Similarity 85.1%; Pred. No. 1e-20; Matches 120; Conservative 0; Mismatches 21; Indels 0
                                                                                                                                                                                       75.1%; Score 107.4; DB 3; Length 165; 85.1%; Pred. No. 1e-20; tive 0; Mismatches 21; Indels 0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 7, Application US/09276625

Patent No. 6435392

GENERAL INPORMATION:
APPLICANT: Engelhardt, John F.
APPLICANT: Duan, Dongsheng
TITLE OF INVENTION: Adeno-associated virus vectors
FILE REFERENCE: 875.001081;
CURRENT APPLICATION NUMBER: US/09/276,625
CURRENT APPLICATION NUMBER: US/09/276,625

CURRENT APPLICATION NUMBER: US/09/276,625

NUMBER OF SEQ ID NOS: 13

SOSTWARE: FastSEQ for Windows Version 4.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          125 GCGCAGAGAGGAGTGGCCAA 145
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Patent No. 6897045;
GENERAL INFORMATION;
APPLICANT: Engelhardt, John F.
APPLICANT: Duan, Dongshen
SEQ ID NO 1
LENGTH: 165
TYPE: DNA
ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                Matches 120; Conservative
                                                                                                                                                                                                             Sest Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TYPE: DNA
ORGANISM: Unknown
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                US-10-054-665A-7
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LENGTH: 165
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   US-09-276-625-7
                                                                                                                                   ; OTHER INFORM
US-08-471-914-1
                                                                                                                                                                                          Query Match
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Patent No. 6057152

GENERAL INPORMATION:
APPLICANT: Samulaki, R.
TITLE OF INVENTION: RECOMBINANT VIRAL VECTOR SYSTEM
FILE REFERENCE: 6636-007

CURRENT APPLICATION NUMBER: US/08/471,914A

CURRENT FILING DATE: 1995-06-06

EARLIER FILING DATE: 1995-05-15

NUMBER OF SEQ ID NOS: 13

SOFTWARE: Patentin Ver. 2.0
                                                      GENERAL INCORNATION:
APPLICANT: Samulski, R. J.
APPLICANT: Xanao, X.
TILLE OF INVENTION:
NUMBER OF SEQUENCES: 6
CORRESPONDENCE ADDRESS:
ADDRESSEE: Pennie & Edmonds
STREET: 1155 Avenue of the Americae
                                                                                                                                                                                                                        CITY: New York
STATE: New York
STATE: New York
COUNTR: US.A.
ZIP: 10036-271
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
SPETION NUMBER: US/08/440,738A
FILING DATE: May 15, 1995
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match 75.1%; Score 107.4; DB 2; Best Local Similarity 85.1%; Pred. No. 1e-20; Matches 120; Conservative 0; Mismatches 21;
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                     Sequence 1, Application US/08440738A
Patent No. 5869305
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NAME: Coruzzi, Laura A
REGISTRATION NUMBER: 30,742
REFRENCE/DOCKET NUMBER: 6636-
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 790-9090
TELEFAX: (212) 869-8864/9741
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TELEX: 66141 PENNIE
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             MOLECULE TYPE: DNA (genomic)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               LENGTH: 165 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TOPOLOGY: unknown
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         US-08-440-738A-1
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US-08-471-914-1
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53 Accertagraficaderresecaerecererereseseceereseresereseses 112
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 6, Application US/09276625
; Sequence 6, Application US/09276625
; Batent No. 643392
; GENERAL INFORMATION:
; APPLICANT: Engelhardt, John F.;
APPLICANT: Engelhardt, John F.;
; TILE OF INVENTION: Adeno-associated virus vectors
; TILE OF INVENTION: Adeno-associated virus vectors
; TILE OF INVENTION: Adeno-associated virus vectors
; CURRENT APPLICATION NUMBER: US/09/276,625
; PRIOR FILING DATE: 1998-03-25
; PRIOR FILING DATE: 1998-05-20
; NUMBER OF SEQ ID NOS: 13
; SOFFWARE: FastSEQ for Mindows Version 4.0
; SEQ ID NO 6
; LENGHH: 272
                                                                                                                                                                                                                                                                            NAME/KEY: misc_feature
LOCATION: 1..152
LOCHER INFORMATION: /note= "Right ITR Sequence in
Patent No. 6038885
OTHER INFORMATION: pXL2384"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         DB 3;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ; TYPB: DNA
; ORGANISM: AAV circular intermediate, clone p1202
US-09-276-625-6
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                                                                                                                                                                                                              TOPOLOGY: linear
MOLECULE TYPE: other nucleic acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    172 GCGCAGAGAGGAGTGGCCAA 192
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        123 GCGCAGAGAGGGAGTGGGCAA 143
    REFERENCE/DOCKET NUMBER: S:
TELECOMMUNICATION INFORMATION
TELEPHONE: (610)454-3839
                                                                  INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
                                                                                                                                         LENGTH: 192 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
                                                                                                                                                                 TYPE: nucleic
STRANDEDNESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     RESULT 13
US-09-276-625-6
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; Sequence 3, Application US/08702573
; Patent No. 6033885
; GENERAL INFORMATION:
    APPLICANT: LATTA, Martine
; APPLICANT: DENEFLE, Patrice
APPLICANT: VIGNE, Emmanuelle
; TITLE OF INVENTION: INTEGRATION THEREOF AND THERAPEUTICAL USES THEREOF
; TITLE OF INVENTION: PREPARATION THEREOF AND THERAPEUTICAL USES THEREOF
; NUMBER OF SEQUENCES.
; ADDRESSEE: Rhone-Poulenc Rorer Inc.
; STREET: 500 Arcola Rd. 3C43
; CITY: Collegeville
; STATE: PA
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US-10-054-665A-7
                                                                                                                                                                                                                                                                                                                                                                                                                                           Score 107.4; DB 3; Length 165; Pred. No. 1e-20; 0; Mismatches 21; Indels 0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               COMPUTER: FLOPY disk
COMPUTER: FLOPY disk
COMPUTER: IBM PC compatible
COPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/702,573
FLING DATE: US/08/702,573
PRIOR APPLICATION DATA:
APPLICATION NUMBER: W 94/02445
PRIOR APPLICATION DATA:
APPLICATION NUMBER: W 94/02445
FILING DATE: 03-MAR-1994
PRIOR APPLICATION NUMBER: W PCT/FR95/00233
FILING DATE: 28-FEB-1995
ATTONREY/AGENT INFORMATION:
NAME: SMITH Ph.D., JULIE K.
REGISTRATION NUMBER: 38,619
APPLICANT: University of Iowa Research Foundation
TITLE OF INVENTION: Adeno-associated virus vectors
FILE OF INVENTION: Adeno-associated virus vectors
CURRENT APPLICATION NUMBER: US/10/054,665A
CURRENT FILING DATE: 2002-01-22
FRIOR APPLICATION NUMBER: US 60/086,166
PRIOR FILING DATE: 1998-05-20
PRIOR FILING DATE: 1998-03-25
NUMBER OF SEQ ID NOS: 14
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 7
LENGTH: 165
TYPE: DNA
ORGANISM: Unknown
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       GCGCAGAGAGGGAGTGGCCAA 145
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Best Local Similarity 85.1%;
Matches 120; Conservative (
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COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
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                         Sequence 6, Application US/10054665A
Patent No. 6897045
GENERAL INFORMATION:
APPLICANT: Engelhardt, John F.
APPLICANT: Engelhardt, John F.
APPLICANT: University of Iowa Research Foundation
TITLE OF INVENTION: Adeno-associated virus vectors
FILE REFERENCE: 875.007082
CURRENT APPLICATION NUMBER: US/10/054,665A
CURRENT FILING DATE: 2002-01-22
PRIOR APPLICATION NUMBER: US 09/276,655
PRIOR APPLICATION NUMBER: US 09/276,625
PRIOR FILING DATE: 1999-03-25
NUMBER OF SEQ ID NOS: 14
SEQ ID NOS: 14
SEQ ID NOS: 12
LENGTH: 272
                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match 75.1%; Score 107.4; DB 3; Best Local Similarity 85.1%; Pred. No. 1.1e-20; Matches 120; Conservative 0; Mismatches 21;
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Pred. No. 1.4e-20;
0; Mismatches 21;
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US-10-054-665A-6
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Patent No. 6916635
GENERAL INFORMATION:
APPLICANT: Hearing, Patrick
APPLICANT: Bahou, Wadie
APPLICANT: Bahou, Wadie
APPLICANT: Gandalon, Ziv
APPLICANT: Gandalon, Ziv
APPLICANT: Gantenko, Dmitri
ITLE OF INVENTION: Adenoviral Vectors
FILE REFERENCE: STONYB-04970
CURRENT FILING DATE: 2001-02-12
PRIOR APPLICATION NUMBER: 60/237,747
PRIOR FILING DATE: 2000-10-02
NUMBER OF SEQ ID NOS: 27
SOFTWARE: Patentin version 3.0
SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TYPE: DNA ORGANISM: Human adeno-associated virus 2
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Best Local Similarity 85.1%;
Matches 120; Conservative (
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RESULT 14
US-10-054-665A-6
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Search completed: November 29, 2005, 14:27:39 Job time : 20.3389 secs